dhlshlb

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- nucleic search, using sw model OM nucleic July 7, 2004, 11:41:13 ; Search time 1883 Seconds (without alignments) 5478.302 Million cell updates/sec Run on:

US-09-437-450A-40

Title: Perfect score:

Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

6940544 Total number of hits satisfying chosen parameters: 3470272 seqs, 21671516995 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

Database :

GenEmbl:*

1: 90 ba:*

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em_sts:* em un:*

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em_htgo_mus:* em_htgo_other:* em_sy:* em_htgo_hum:* em_htg_mam:* em_htg_vrt:*

is the number of results predicted by chance to have a Pred. No.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	90	_	S Ca	31 Caenorhab	979 Dicty	325	.93 Felis c	Ratt	Mus		AP004700 Oryza sat	ory		Stenogep	AC10819C Felis cat	-	cv.		AL935279 Zebraiish	Mus mus	ACII8982 Galius ga	Mouse			AP005066 Oryza sat	ATTECHES DATE DATE OF THE PARTY DATE	ALAKSON HOMO Sani	Humar	Нишап	3 Lemur	1 Oryza	Humar		AC023124 Homo sapi	ø				164		136	440 Rattus n	10610 Fusoba	AL031586 Human DNA
	ΙD	AF301606	CEF35E8	CEK01D12	CEC54D10	AC116979	AC022325	AC108193	AC126197	AC146595	AC108074	AP004700	AP005757	AC132361	AF147831	AC108190	AC130799	AC101022	AC122795	AL935279	AC016983	AC118982	AL672241	AC016982	AC084742	AP005066	AC104363	AL353/69	CNSOCCIS	CNS06C70	AC123543	AC120991	AL138727	AC016733	AC023124	AL772216	AC128949	AC117010	AF038045	AC122164	CNS06CBB	AL445436	7	2	HS324C6
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ALIGNMENTS

Caenorhabditis elegans cadmium-inducible lysosomal protein CDR-1 (cdr-1) mRNA, complete cds.
AF701606
AF301606.1 GI:11120428 RESULT 1 AF301606 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Caenorhabditis elegans Caenorhabditis elegans Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.

1 (sites) Liao, V.H. and Freedman, J.H. Cadmium-regulated genes from the nematode Caenorhabditis elegans. REFERENCE AUTHORS TITLE

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18685 TICGGAIGITCTCGAAAAGGACTICCCAAAGTIATIGGAGTACTGTGAAAGAGTICGTCA 18744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence CETGGC12.

The true right end of clone F35E8 is at 23602 in this sequence. The true left end of clone T05G11 is at 1324 in this sequence. The true right end of clone T05G12 is at 104 in this sequence. The start of this sequence (1. .104) overlaps with the end of sequence CETG6C12. The end of this sequence (23499, .23602) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 TGAAGTTTACCCAAAGGACTTTACTATGTGAATTAAATTGTCAAACTAGTAGTCAGATCA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Nov 29, 1997 this sequence version replaced gi:2546904. Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (06-WOV-1996) Nematode Sequencing Project, Sanger
Institute, Hinxton, Cambridge CBIO 15A, England and Department of
Genetics, Mashington University, St. Louis, MO 63110, USA. B-mail:
jesssanger.ac.uk or rw@nematode.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

For a graphical representation of this sequence and its analysis see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMPORTANT: This sequence is not the entire insert of clone F35EE It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
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                                                                                    Caenorhabditis elegans
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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The true left end of clone F35E8 is at 18616 in
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                                                                                                                                                                                                                                                                                                                      The C.elegans Sequencing Consortium. (bases 1 to 23602)
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/strain="Bristol N2"
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/clone="F35E8"
                                                                 Caenorhabditis elegans
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ADSDLIEMRLRSHFKIPSLETQSVALSKFADHHLFFVLIRFKIAVDEFYKTIIE
IIGLPTFINFILMPLLKAIISKNYNKCQGAIGDPELSELDEILHRDLAIVENTLAKK
                                                                                                                                          Liao, V.H.C., Dong, J. and Freedman, J.H. wholevilat Characterization of a Novel, Cadmium-inducible Gene from the Nematode Caenorhabditis elegans. A NEW GENE THAT CONTRIBUTES TO THE RESISTANCE TO CADMIUM FOXICITY
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'procein id="AAG30870.1"
'db_xref="GI:11120429"
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  dentification and cloning of new cadmium-responsive genes
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                             differential display
J. Biol. Chem. 273 (48), 31962-31970 (1998)
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/evidence=experimental
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Location/Qualifiers
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/translation="MYGKGFQYPPINV2VSPVFQAFYDCIYPKLEPYKGQYKEFWFAF
TNVTKQCDNLEVYKSMDIHPASNRGETKYVALFKTNELLIWTLGITBOFGAEYKLKE
LIPRALDFFGADPAAYTKOLYEPYTGGKYFQYAVGGESGWGRSVYEKDPYGEYYKE
VKADYFFKNILLAFKTELDELMIDVBQW3YFILDQIHRWBAIDKBGILLGQINVBLEHGEI
FGEVEDQMKKLHDFVWRLLDEKRYVMMKPHFVLYKMVGFIRVFRWNVSDKECADLFVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /standard name="K01D12.3"
/note="contains similarity to Pfam domain: PF01482 (Domain
of unknown function), Score=202.1, E-value=2.8e-57, N=1"
                          NEEGDDVPVEGTPFFKAFYNCYYPKIASLRCNYEMFWTSFVNI-TKECDGLEEYKALDI
QPVANTDEVKYVAFPKRDENITMYTLGIGHDVDAEMRIKKLIRPKFGVDPSPEINK
DLYEVKLGGNYFQIAVSGKGGMQKSYIFRKEYRDEATWHIGADYFFGDMLQKPRVDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPATHTOT PLIATUSYQUNQQAHGSQQHHTPPHQQGQMFNPIHPHGIIGACSNSA
QQCSSTNSYIPIQTATVSIPTFNGEILHFQSFMELFNTLIDSQPIAEIFNIKNESLOQ
IQQUMTECVSIFNQCKIQPPANNYMAINIITSKLPRRYIKRIYFGHRDDYLABEIL
EWYRSTIQTDFITAUNAEAHQYSKYNYESLQPELKNSYTGNNYQLEEIHFSKYT
HPPLRYQHHLQNGYNTSIAERTDQQPLYBPTSEHHLASSTAVEIKTNINEKTAKVPP
IVEIPKQNKNQSRGSNYETLLQVYSLISVLEEIHGSGYTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BINNEGESPDAMEKYGOSRICFSSEKHSTTTHYTPAEESHNFGFNLHVLDHKITTGWQ
DDKHPWDPGTQQRYQLAPRIQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'tränslation="MFSIKSVIANIETSFQVRQSTQKRRRWQTNQHLCQSMQSEITKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILTLILTINCSEKNHOKPVQVQPKQPLHRLRLQPQPHQNILQHLPQPLESTNTRSRR
                                                                                                                      MMDTEGNEFPVLDMIHRGGPLDQRGVTICQMNIBIHKOLMKDITGEREKFHDFVWKLL.
ADKKYIMVKPPYVYWFHQPIRTVIINVADPECTNLYMN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INEDEFEIIPMETIISSNEIGNQIDVEDSQQLDSKDQYQKVSELQDDFIETVETKSIT
translation="MITSMPYNRLREAILHKRKCSKHILVAMVLISSMLLLINIMQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(11177. .1144,11518. .11592,11643. .11801,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MHKSRSPDQVDYPPFPVSVLSTDSIVPECNINSTTQDSVPQYSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           jōin(8020. .8048,8312. .8399,8466. .8585,8629. .8697,
8747. .8888,8932. .9314}
/gene="K01D12.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(8020, .8048,8312, .8399,8466, .8585,8629.
8747, .8888,8932, .9314)
/gene="KOlD12.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="K01D12.15"
standard name="K01D12.15"
note="cDNA EST yk16399.5 comes from this gene
                                                                                                                                                                                                                                                                                                              /standard_name="KOID12.2"
/standard_name="KOID12.2"
/note="CONA BST yk2e11.3 comes from this gene
CDNA BST yk2e11.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNNA BST ykl6599.3 comes from this gene CNNA BST yk2667.3 comes from this gene CNNA BST yk2667.3 comes from this gene CNNA EST yk26189.3 comes from this gene CNNA EST yk11811.3 comes from this gene CNNA EST yk11811.3 comes from this gene CNNA EST yk26649.5 comes from this gene CNNA EST yk26649.5 comes from this gene CNNA EST yk279812.5 comes from this gene CNNA EST yk211811.5 comes from this gene CNNA EST yk411811.5 comes from this gene CNNA EST yk411811.5 comes from this gene CNNA EST yk411811.5 comes from this gene CNNA EST yk552911.3 comes from this gene CNNA EST yk552911.3 comes from this gene
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/protein_id="CAA99878.2"
                                                                                                                                                                                    complement (join (6025. .7139,7192. .7646))
                                                                                                                                                                                                                                                  complement (join (6005. .7139,7192. .7646))
                                                                                                                                                                                                                                                                                                                                                                                                                                                 codom_start=1
/produci="Mypothetical protein K01D12.2"
/protein id="CAA9870.1"
/db_xref="G1:3878144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Hypothetical protein K01D12.3"
/protein_id="CAA99877.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oin(9968. .10033,10136. .10426)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'db xref="GI:3878151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="K01D12.15"
join(9968. .10033
                                                                                                                                                                                                                        /gene="K01D12.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                overlap between neighbouring submissions.
This sequence is the entire insert of clone KOLD12. The true right end of clone FS3H12 is at 4908 in this sequence. The start of this sequence [1. .102) overlaps with the end of sequence 374472.
The end of this sequence (32761. .36974) overlaps with the start of
             18745 IGAAGTITACCCAAAGGACITIACTATGIGAATIFAATIGICAAACTAGTAGTGGATCA 18804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
                                                                                                                                                                                                                                                                                             linear INV 10-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (29-JUN-1996) Nematode Sequencing Project, Sanger Institute, Hinkton, Cambridge CBIO. 158, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Mashington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

For a graphical representation of this sequence and its analysis see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .1318,1365. .1564,1640. .1828,1874. .2015,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .1318,1365. .1564,1640. .1828,1874. .2015,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                             CEKO1D12 36974 bp DNA linear INV Caenorhabditis elegans cosmid K01D12, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Nematoda, Chromadorea, Rhabditida,
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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/protein id="CAA99867.1"
/db_xref="G1:3878141"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.elegans Sequencing Consortium.
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/strain="Bristol N2"
                                                                                                                                                                                                                                                                                                                                                                                                                             protein.
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/chromosome="V"
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/gene="K01D12.1"
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/gene="K01D12.1"
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                                                                                                                                         18805 ATAAATTTAACGTGG 18820
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Caenorhabditís elegans
Caenorhabditis elegans
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                                                                           210 ATAMANTICIACGIGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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IMPORTANT: I
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CEKOID12/c
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TITLE
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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.8697,

INV 03-DEC-2003

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IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be storter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone C54D10. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence CEF28C1.
The true left end of clone F28C1 is at 40353 in this sequence. The true right end of clone K01012 is at 4214 in this sequence. The start of this sequence (1. .4214) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The end of this sequence (40353. .40450) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitteed (29-UTM-1996) Nematode Sequencing Project, Sarger
Institute, Hinxton, Cambridge CB10 ISA, England and Department of
Genetics, Mashington University, St. Louis, MO 63110, USA. E-mail:
jessanaper.ac.uk or rwantmatode wastledt
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note: For a graphical representation of this sequence and its analysis see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                               34736 CIACAGIRCIGIGARAGARAICCGARAGGARAITIRICCARAIGAITITRACTAITIGA 34680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neighbouring submissions.
The true left end of clone C54D10 is at 1 in this sequence. The true right end of clone C54D10 is at 1020 in
                                                                                            124 TIGGAGIACTGIGAAAGAGITCGICAIGAAGITTACCCAAAGGACTTTACTAIGIGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Current sequence finishing criteria for the C. elegans genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                        CEC54D10 40450 bp DNA linear INV Caenorhabditis elegans cosmid C54D10, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism=™Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The C.elegans Sequencing Consortium.
2 (bases 1 to 40450)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                           Z75531.1 GI:1418465
HTG; Serine protease inhibitor.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strain="Bristol N2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               available information.
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VERSION
KEYWORDS
SOURCE
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TITLE
JOURNAL
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TITLE
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                                                                                                                                                                                                                                                           RESULT 4
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TREENINVIADEGHHAPAQQGHSESPEPPSPFWINPKPVLSYGAANFLANLPPAQGY
YGAPIDSSHRGYDGFSLSAPAPSGSSASVDOTKFALARALDANTRRRHRI.
Complement (join (22649. .22891.22850. .23341,23437. .23753,
23798. .24207,24280. .24377,24429. .24458))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCCVLFTNLFLERLUTGNSYTLRSLRERKTRYRLAGSGNKPVTLLLNNBDFNESSSS
CGGHMONMRPSVYKVPFILFSMCLVLITASAGIYSVVENMYIDSLYFCFISFATIGF
GDVYSNQDVTRNSPDLYRFVNFCLLTLGACFFYCLSNVSSIVVRQLLNMAIKRADVK
VEDRSFLCFKKKRYRGLGLRPPKGISNLAGDNCCIBHLNVFRIRYDI"

join (21543 . 2227, 22273 . 22403)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="ymklopargiggremlrantlesitrakygcparlriyeenarf
Vliciiilyylafgailfhwleweneyderlaidnrmadygkyyckhkplnecdfeem
Vrfisdaatsgllnsrsrphlgslffsatyistigfgtstprthlgrfiivygyyg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAA99872.2"
/db_xref="G1:31441821"
/translation="MGRQGSLALLLSIILIGETIANEYDGLSSHQSHQSTVTSAPIHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQQTSRNRPYNQPQLQQKESVLTQSYQVLPBSRNYYQYPQYLFTHTGYSNLQTVGQP
YQMYGSAPGSNVVSGGNSESYGYNQQAPVPTVAPAPVHFSBRQRSYSAAPTPPSPFSB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(22649. .22801,22850. .23341,23437. .23753,
23798. .24207,24280. .24377,24429. .24458)}
/gene="KOlD12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /crānslation="MTSYLMQSLPGGIKMNEIITKRTVLSVAAGIGIGIVFANFVRYW
RQKREAKVPQSIIEEIGKDADIIVPSAPSLRRSQSGRGMRPPSSQGERSSLRNSIRQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQRSMNPIEADITSGQELCTELRKTIEKVHHNLEMVKORSSKOMERSIKIEGILKGLK
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NEBQLRQDVBGRCYCETGFYDVAIDFIILDAFEDLKSPPSAVYSVTKUYFNSMSMKYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVEDEIVLLVPQMEDFRDDNMEFYSVSGGSGYAGSVRTGRSRTLSVLSDDSFRSAVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FACDIDDIDFVSDAANLDKNELRFLDEGMQAALNGEVKYRKSRMEFCKCDSETDFAAK
                                                                            complement(join(11177. .11444,11518. .11592,11643. .11801,
11987. .12085,12159. .12481,13776. .13919,14219. .14302))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                   .12085,12159. .12481,13776. .13919,14219. .14302))
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                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="C. elegans TWK-14 protein {corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /standard_name="XO1D12.5"
/note="cDNA EST OSTF168B6_1 comes from this gene
cDNA EST OSTR168B6_1 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
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                                                                                                                                                                                               /note="similar to potassium chance protein cDNA EST yk743d10.5 comes from this gene cDNA EST yk743d10.3 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard name="K01D12.6"
note="cDNA EST cm1496 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA SST YK384f1.3 comes from this gene CDNA SST YK384f1.5 comes from this gene CDNA EST YK1046e01.5 comes from this gene CDNA EST YK1046e01.3 comes from this gene CDNA EST OSTR196f4 comes from this gene CDNA EST OSTR196f4 comes from this gene CDNA EST OSTR196f4 comes from this gene
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/product="Hypcthetical_protein K01D12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon start=1
'product="Hypothetical protein K01D12.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oin(21543, .22227,22273. .22400)
gene="K01D12.5"
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0; Mismatches 5
                                                                                                                                                                            name="K01D12.4"
                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAA99871.1"
/db_xref="GI:3878145"
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/db_xref="GI:24817517
                                                                                                                                                                                                                                                                                                                                                        sequence K01D12.4)
                                                                                                                                               /gene="twk-14"
                                                                                                                                                                            standard
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Score 95.4; DB 3; Length 40450; Pred. No. 8e-15;

40.18;

Query Match Best Local Similarity

ORIGIN

34856 TATTTATTTGGASACCACATTGCTCCAGTTGATGCGACGCTTTTTAGCCAGTTGGCAGTT 34797

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64 GICIALLAICCATICCGCAAICACAITICGGAIGIICICCGAAAAGGACIICCCAAAGIIA 123

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IIRKVIQDMHHLMSVRHKNIQASNIAGKLLDSSSSSNSNLQFSLSSSFIFSSSSNNTT
TFTQXDQDQFNDDKISGDEIFFFINMSKYLEKEDKKDQLIQKDEEIILKTFNDNNN
NIMANNINNINNINNINIININNDNDNNNNNKNIDNKGYLBNINNNNADKIEKLSPVN
NINKGNSEIEKNIEKLKNINNINNVEINBALISIIKRTCKNIPSSSFSSVKNLKRSPPS
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FDTIVTELGEDDI PKOTOLNILTLECYFSNEQKYETTNPYLKDLSNLSDPIKILKTLN
LITONLKOHNEPFEQQYRDPNICMVSRFSGYLSSWVYSPKVVQPLSFYETGSSLMILX
ELPYQNDHFVNMLVKGGLPFANGGENGSTCPDIIKQFFSFCAYLASDAQKDLKTIYSR
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PIKCNLKGKISMDVHQSAVDCIHRIVSYKKKTLNRLPYKWSELMSALFSLISMVSTLK
ISNDKIQLNQSIHVGISTVNIFNLFINYGDSFLPSPNDYDELFYEIIRSGQVIENFYQ
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QLINIRSIVQHFTSKLEEWSANNAEVALTAPQVSKIIKDNYDTLRLKLQENLDQFEPY
VENPKEVLFFKHIIKELINJLRKQINVTNII"
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GNNNNNNEQDNDLQEKEQNELSDDSDVEGFEIIFNNNNIYSHDVSLCFPIDLVCRVTL
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                                     /tränglation="mdQfKVPPPTXAPVAGQTIYGAPSYNNYYMRTPQVSTAPMIYPT
PMAZPEINTPPIMTQPIMTPPMKYPPIIPSQPFMGPSKVSPINSPENIPSQPFMGPSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                      YLIKSAEPIYEDSIIILGDYYYNGFKTIDNHDDHDDGSGENEELALIQDYFKAFNLF
KIGASLAVDSNSLTKLGICFYYGRGYTIDYNEAYRLFYQSSICDHHQEHQEHVFEITFYYL
GLCLFYGKGYLKNQCKGFEYFMKSASLNHYSPALEAVGRCFLNGEGISQNFMQAKLYF
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HCPTHDEPIIKYCILCNCVICNLCEKTTHFHNNNNQINITQFPWIPKKKSKSIEBLEL
                                                                                                                                                                                                                                                                                                                                                                      NEI DEYNNIYNINI NIKINININIKKINIVINIVINIKINIENKEI NEI HEITHENKAQRSINSPPLPK
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AQCILGSSYYYGMIGYSVNFEKSLKYLTKSABQNIAKAY FELFNYYKQOKKDLIKSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein id="AAOS221.1"
db xref="G1;28829706"
'translation="MEIDKAVEQSSNKVEYNQPKSPITSILVNNNSSNNNNNNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(9007..10431)
/note="GeneID exon scores (in order of location ranges):
177.93 - GSCJ ID dd_03414"
/codon_start=1
                                                                                                                        2839. .4479 /note="GeneID exon scores (in order of location ranges):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="GeneID exon scores (in order of location ranges):
34.62, 63.42, 31.78, 100.55 - GSCJ_ID dd_01261"
/codon start=1
/product."hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="GeneID exon scores (in order of location ranges):
50.22 - GSCJ_ID dd_02577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'product="similar to Plasmodium falciparum. Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (join (4673. .5239, 5354. .6118, 6205. .6621,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NHQKNYYKQEIDNTNIKNIKCKQDSLIDKTFNKVNYLN"
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/protein_id="AAO52220.1"
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protein id="AaM34303.2"
db_xref="G1:28829708"
                                                                                                                                                                              88.56 - GSCJ ID dd_01260"
/codon_start=1
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/db_xref="GI:28829707"
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complement(11849. .12583)
                                                                                                    /SPGYGVTPNLNVPFSTNVKYYD"
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Dictyostelium.
Eukaryota, Mycetcoadeum
1 (bases 1 to 88549)
Gloeckher, G. Eichinger, L., Szafranski, K., Pachebat, J., Dear, P.,
Lehmann, R., Baungart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K.,
Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany on Mar 4, 2003 this sequence version replaced gi:20042934. CGS predictions from GeneID do not necessarily reflect true genes. Further Information is available from IMB Jena, Department of
                                                                                                                                                          64 GTCTATTATCCATTCCGCAATCACATTTCGGAAAAGGACTTCCCAAAGTTA 123
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                                                      chromosome 2 of Dictyostellum discoideum (2002)
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Biotechnology, Beutenberstr. 11, Jena 37745, Germany
3 (bases i to 88549)
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and the Univerity Colonge, Institute for Biochemistry
(http://www.uni-koeln.de/dictyostelium/project.shtml
Indels
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/mol_type="genomic DNA"
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/map="6357117-6445670"
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Homo sapiens BAC clone RP11-391J13 from 4, complete sequence.
ACU22325
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Submitted (09-MAR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                    117 AAAGTTATTGGASTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTAT 176
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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The sequence of Homo sapiens BAC clone RP11-391J13
Unpublished
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University, 4444 Forest Park Avenue, St. Louis,
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Park Avenue, St. Louis,
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
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Genome Res. 8 (11), 1097-1108 (1998)
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       58.7%; Pred. No. 1.5; tive 0; Mismatches
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Sulston, J.E. and Waterston, R.
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University, 4444 Forest
6 (bases 1 to 193057)
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Waterston, R.H.
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join(22686. .22743,22820. .22926,23004. .23139,23232. .23558,
23639. .27180)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Crotein id="AA052223.1"
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DSIDRXTSPVYIPTDQDILHTRVWTRGVHETNFEIGKIKFRLYDVGGQRSERKKKLSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mmrnihlyifvslilslingiksikvgngdfsvyditdsfddlu
tlyndoysiggldenifwlkvintvgigenokfnlllltldnsttigeddfftltcker
pvnierelvgcklfidkqykgrygilvhniglegylsvbglennfisntfsmyfydds
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LSYYDRYTYRTYFIRMYD SKRTNITYSIKMYROLTTYGFASENITTQPSSIKYFIS
SETKRAIVDTHIVGVI.NKYRSIETEKIDDACFSSESGOYISIQIPNYKTSVELDPNFSVLL
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VKKNFTCPCVQDFSFITERNSLLANNNNNNNNNNNNNNNNNNNNLYSKATLSQMLSS
SPENSY I LAFYNSBYSVCHYNNQNYGISYSTGSVLYNBNGVSVYVVDDQSNQSILFHC
ONDQCVQSFIDISCDMPPNDLQIYCN"
                                                                                                                                                                                                                                                                                                                                                                                                                             FSIAVGƏCLPIBGYLSYVINDMPPTTMKFITMGGNGNSFILKQYDSQDQWCKQDPINT
LQPDN=DTCVEQEAFINVNNSLLADTPVVYSKLFISQNVPTYAPDSVIIGQYNTNTNV
CTYNDQQFGVSYTSGTVIYNENGISIHVLCNQVNQSNMFKCKESKCGETFIDTYCQMS
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SLPFLNNTYIVFDLKQYRNINDTNCQIYITNQLGFSSNEINFVLKAHTNVTMPFTTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 esskienstchknosgliktoligiigstagfililivisivykksttleninra
                                                                                                                                                                                                                                                                                                                                                                                             'Lranslation="MKLLLTL1L1UNYCCFINANKLFVNFWSSYSSNTCDGNPSGIG
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FREKIKHVDLSETFPEYKGGRDYERASNYIKERFWQINKTEQRAIYSHITCATDINNI
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Dehydrogenase, succinatesemialdehyde dehydrogenase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="similar to Dictyostelium discoideum (Slime mold). Guanine nucleotide-binding protein alpha-2 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="GeneID exon scores (in order of location ranges): 4.93, 3.57, -1.17, 18.69, 174.64 - GSCJ_ID dd_01857"
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/note="GeneID exon scores (in order of location ranges):
218.38, 14.76 - GSCJ_ID dd_01858"
                                                                                                                                                              /note="Geneine zon scores (in order of location ranges): 57.23 - GSCJ ID dd_02576" (codon_start=1
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/note="GeneID exon scores (in order of location ranges/:
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protein id="AAO52224:1"
db_xref="G1:28829711"
                                                                                                                                                                                                                                                                                 product="hypothetical protein"
protein id="AAM34304.2"
db xref="G1:28829709"
                                                                                                                                                      .13840)
                                                                                                                                                   complement (13151.
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CDS

SGS

/rpt_family="ERV1"

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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we oily sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30;; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Mashington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor; as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B., Tatrono, M., Caranese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Generals 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Carcer Institute (http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-627C20; the clone sequenced to the right is AC036161. Actual start of this clone is at base position 1 of RP11-391J13; actual end is at base position 193057 of RP11-391J13.

FEATURES

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Location/Qualifiers
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/rpt_family="ERV1"
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/rpt_family="Ll"
9379. .10523
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1160. .3193
                                                                                                                                                                                                                                           /chromosome="4"
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repeat_region

rpc_ramıı 392613	rpt famil	famil	rpt_famil	16 Famil	6009. 16	3516	rpc_ramil 641716	/rpt_family="L1" 1890918931	rpt_raml. 893319	/rpt_family="MaLR" 2186722184	/rpt_tamily="Alu" 2395124020 /	/rpt_ramily="\IA\n" 2402124244	/rpt_tamily="MEK2_type" 24240, .24685	/rpt_tamily="MEK2_type" 2644726542	/rpt_tamily="(TATATG)n" 2654326692	/rpt_family="L1" 2675726865	/rpt_family="Tc2" 2709627177	/rpt_tamily="AT_rich" 2720027801	/rpt_family="L1" 2793928875	/rpt_family="L1" 2889428962	/rpt_family="ERV1" 2895829193	/rpt_family="ERV1" 2919429604	/rpt_tamily="Malk" 2960530035	/ rpc_ramily="EKVi" 3004630184	/rpt_tamily="L1" 3019530264	/rpc_ramily="Ekvi" 3026530971	/rpt_ramily="Li" 3097031312	/rpt_ramily="Ll" 3131331606 /	3160731793.	/rpt_ramily="bl" 31820, 32609	/rpt_ramily="bkvi" 3263532946	/rpc_ramily="b1" 3295933735 /	/rpc_ramily="Li" 33740, .34204 /	/IDC_Idmily="Li" 3420534236 /rnt familv="(/a)r"	4237. 34403	rpc_ramiry= 4404 3470
repeat region				repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region		repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat region

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41781 TITGCITCTCTCAGATACACTITCCTGTTACAGTTATGGGATAGTCACAACACCTATTTC 41722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 TIGGCRACTGTCTATTATCCATTCCCCAATCACATTTCGGATGTTCTCGAAAAGGACTTC 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="clone overlaps with GenBank Accession Number AC108899 clone RP86-261015 (center project name cof)"
                  Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0:990319
Consensus quality: 138634 bases at least Q40
Consensus quality: 138674 bases at least Q30
Consensus quality: 138677 bases at least Q20
Insert size: 133000; agarose-fp
Insert size: 133683; aum-of-contigs
Quality coverage: 12.26x in Q20 bases; sum-of-contigs
Quality coverage: 11.76x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC108190 clone RP86-44312 (center project name cod)"
58366. .138683
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1. .61312
/note="clone overlaps with GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                   consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 ATGTGAATTAAATTGTCAAACTAGTAGTCAGATCAATAAAATTCTACGTGGCA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 105452: contig of 105452 bp in length 105453: 135522: gap of unknown length 105553: 138683: contig of 33131 bp in length.
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16.9%; Score 40.2; D3 2; Length 138683;
Best Local Similarity 52.0%; Pred. No. 2.4;
Matches 90; Conservative 0; Mismatches 83; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC126197.5 G1:30579275
HTG; HTGS_PHAS31; HTGS_EVLLTOP.
with a Phrap-derived quality score.
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                     52727 Sicalicallakoncicacallifiliticicakaalikongsalaakoliokolkaaal 52668
                                                                                                                                                                                52787 AACAGCCAATCATATGGGGATTATACAATICCAAAATACTATTAAAGCTATTCCTTAA 52728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC108193 138683 bp DNA iinear HTG 28-NOV-2002
Felis catus clone RP86-469M9, WORKING DRAFT SEQUENCE, 2 ordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Akther, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S. M., Senjamin, B., Blakesley, R.W., Bouffard, G., Brinkley, C., Brooks, S., Carjamin, B., Blakesley, R.W., Bouffard, G., Brinkley, C., Brooks, S., Carjan, K., Coleman, B., Baghe, M., Granite, S., Guan, X., Gupta, J., Hansen, N., Ho, S.-L., Idol, J. R., Karlins, B., Laric, P., Lee-Lin, S.-C., Legaspi, R., Maduro, Q.L., Maduro, V.B., Paguirigan, C., Rasson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K., Schneler, M.G., Sison, C., Stantripop, S., Thomas, P. M., Trouchman, J. W., Vogt, J. L., Nerberby, K.D., Miggins, L., Young, A. and Green, E.D.
                                                                                                                       60 AACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTTCCCAAA 119
                                                                                                                                                                                                                                               120 GITATIGGAGIACIGIGAAACAGIICGICAIGAAGIIIACCCAAAGGACIIIACTAIGIG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
1 (bases 1 to 138683)
                                                                                                                                                                                                                                                                                                                                                                                                                             52667 TATGAAATTTACAATCTTTATGAAAAGTACAAAAGGGAAAGGTTGAGAACCACAA 52611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-guality ends of sequence contigs have been trimmed away, and each base is associated
                                                                                                                                                                                                                                                                                                                                                                 Submitted (26-JAN-2002) MIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 138683)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (28-NOV-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Nov 28, 2002 this sequence version replaced gi:18376892.
                                                                  Gaps
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   Score 41, DB 9, Length 193057;
Pred. No. 1.4;
0; Mismatches 85, Indels 0;
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Center code: NISC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: nisc_zoo@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: 469M08
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HTG; HTGS PHASE2; HTGS_DRAFT.
Felis catus (cat)
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      17.2%;
52.0%;
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         Query Match
Best Local Similarity
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AC108193/c
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                                                                                                                                                                                 Carges 1 to 2204/1.

RR Narry, D.Marte, Matrker, M.Lee., Abramzon, S., Adams, C., Allen, H., Abribrokas, S., Amin, A., Angulano, D., Anjen, M., Angulano, D., Banden, H., Balano, D., Anjen, M., Barte, M., Barte, D., Barden, M., Barnstaad, M., Benahmed, F., Barden, M., Barden, M., Barden, M., Barden, M., Barden, M., Carter, M., Edgen, C., Dard, S., Dum, A., Duthin, K., Duval, B., Baves, K., Earnand, C., Cockerl, S., Dum, A., Duthin, K., Duval, B., Baves, K., Earnand, C., Cockerl, S., Dum, A., Duthin, K., Duval, B., Eaves, K., Earnand, C., Cockerl, S., Dum, A., Duthin, K., Duval, B., Eaves, K., Earnand, C., Cockerl, M., Edgen, C., Ramilcon, C., Hamilcon, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of Molecular and Human Generics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030 USA on May 13, 2003 this sequence version replaced gi:24942206. The sequence in this sasembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (04-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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   Rattus norvegicus (Norway rat)
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3 (bases 1 to 250470)
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Direct Submission
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                                    Rattus norvegicus
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SOURCE
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TITLE
JOURNAL
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REFERENCE AUTHORS TITLE JOURNAL

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REFERENCE

COMMENT

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in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgum sequence reads. Both end sequences and whole genome shotgum sequence only contigs will be indicated in the feature table.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html)

* NOTE: This sequence may represent more than one-clone.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 TCCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 AATTGGCAACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus quality: 240374 bases at least Q40
Consensus quality: 243949 bases at least Q30
Consensus quality: 245059 bases at least Q20
Estimated insert size: 254162; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248046: contig of 248046 bp in length 248146: gap of unknown length 249193: contig of 1047 bp in length 249293: gap of unknown length 250470: contig of 1177 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78;
                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                         Center: Baylor College of Medicine
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center clone name: CH230-145E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: Atlas 3.0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: GMMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="CH230-145E6"
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1. .250470
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238284, .240199
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241389. .245579
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145250 ATATCGAAACTATTCTAGTGTTTTTGTCAAATTCTACTGAGAAAGTATTTAGGGTTTAA 145191
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Submitted (20-MRR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 20, 2002 this sequence version replaced gi:18702446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRI 20-MAR-2002
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Direct Submission
Submitted [19-FRB-2002] Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Parkway, St. Louis,
                                                                                                                                                                                                                                        75 ATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTG 134
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                            135 TGAAAGAGTTGGTCATGAAGTTTACCCAAAGGACTTTACTATGTGAATTAAATTGTCAAA
                                                                                                                                                                                               Gaps
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AC108074 AC024668
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                                                                                                                                               Score 39; DB 2; Length 177864; Pred. No. 4.9; 0; Mismatches 75; Indels 0;
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The sequence of Homo sapiens BAC clone RP11-717H13
Unpublished (2001)
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Contact: sapiens@watson.wustl.edu
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Sulston,JE. and Weterston,R.
Toward a complete humar genome sequence
Genome Res. B (11), 1037-1108 (1998)
/note="assembly_name:Contig15"
175174. .176585
/note="assembly_name:Contig7"
176686. .177864
                                                                                        /note="assembly_name:Contig9"
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Drafting Center: WIBR
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5 (bases 1 to 128635)
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Direct Submission
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                                                                  AC146595 177864 bp DNA linear 3TG 06-SEP-2003
Mus musculus chromosome UNK clone RP24-164G18, *** SEQUENCING IN
PROGRESS ***, 6 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (06-SEP-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomī;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 177864)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Mashington University Genome Sequencing Center Center code: WIGSC
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1586: gap of unknown length
24281: contig of 2565 bp in length
24381: gap of unknown length
60849: contig of 36468 bp in length
175073: contig of 114124 bp in length
175173: gap of unknown length
175185: contig of 1412 bp in length
176585: contig of 1412 bp in length
176685: gap of unknown length
176685: gap of unknown length
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Sequencing vector: plasmid, 100$
Sequencing vector: plasmid, 100$
Chemistry: Dy-primer ET; 0$ of reads
Chemistry: Dye-terminator Big Dye; 1008 of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 175407 bases at least Q40
Consensus quality: 175803 bases at least Q30
Consensus quality: 175912 bases at least Q20
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Center project name: M_BB0164618
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/note="assembly_name:Contig13"
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/db_xref="taxon:10090"
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/clone="RP24-164G18"
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Yns musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                          Unpublished
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This seguence may not represent the entire insert of this
                                      clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subcione; and the assembly was confirmed by restriction digest.

family="AT_rich" ..15008

rpt ij,

family="Alu"
. .14067

rpt_f 4025. 4979.

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family="Alu"

.13635

family="L1"
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/rpt_family="L1" 152_ .10608

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family="AT_rich"

.20238

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family="L1"

.20932

. .24745 family="L1"

25029

family="L1"

.23419

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPhersor, Department of Genetics, Mashington University, St. Jouls MD. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org SOURCE INFORMATION: VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RPI1-384DIO, 2000 bp overlap; the clone sequenced to the right is RPI1-766L18. Actual start of this clone is at base position 12191 of RPI1-384DIO; actual end is at base position 717FI13.

Data from AC027411 was used to finish this clone, AC108074.

The sequence of AC024668 has been incorporated into AC108074. Location/Qualifiers

source FEATURES

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organism="Homo sapiens"
                        /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="4"
                                                                                                                                                746. 311 / rpt_family="(TA)n" 829. .1006 / rpt_family="(TA)n" 1007. .1010
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                                                                           clone="RP11-717H13"
                                                                                         /clone_lib="RPCI-11"
7. .317
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275_ 1770
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2046. .2066
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0937_3133
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/rpt_family="ERVL" 6486. .6619 /rpt_family="ERVL" 8484. .8649

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'rpt family="L2"

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'rpt_family="L1"

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43382. .45504
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85233. .35457
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7609. .27719
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128424 TGTCAAACATTTTGAAACGGAGGGAATATAAGGGATTTTAACTTTTTACTTATACTGTTT 128365
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Mus musculus chromosome UNK clone RP24-149E13, WORKING DRAFT
SEQUENCE, 13 unordered pieces.
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2 (bases 1 to 147655)
2 sasakir., Matsumoto, T. and Katayose, Y.
Direct Submission
Submitted (18-SEP-2002) Takuji Sasaki, Mational Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mil: Easaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
On Sep 25, 2003 this sequence version replaced gi:23200616.
The orientation of the sequence is from T7 to SP6 of the PAC clone.
                                                                                                                                                                                                                                                                                                                      APD05757 147655 bp DNA linear PLN 26-SEP-2003
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 8,
PAC clone:P0413H11, ccmplete sequence.
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                                             133 TGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGAATTAAATTGTCA 192
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
O; Gaps
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/organism=^cryza sativa (japonica cultivar-group)"
/ordl_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref=freaxon:39947"
/clone="P0413H11"
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Oryza sativa nipponbare(GA3) genomic DNA, chromosoce 8,
clone:P0413H11
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Local Similarity 60.4%; Pred. No. 5.6;
Loc 54; Conservative 0; Mismatches
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AP005757.2 GI:35764583
     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a "working draft, sequence."

* This sequence will be replaced

* This between the replaced

* This between the replaced

* The finished sequence as soon as it is available and

* the accession number will be preserved.
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1; Poales; Poaceae;
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                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, PAC
clone:P0518H02
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| mol type="garonic DNA"
| Cultivar="Nipponbare"
| Ab_xref="taxon:39947"
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                                                                                                                                                                                                         ch: 16.3%; Score 38.8; DB 9; Length 128635; I Similarity 55.1%; Pred. No. 5.7; 7; 76; Conservative 0; Mismatches 62; Indels 0;
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Oryza satīva (japonica cultivar-group)
Stryca (yaridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
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2 (bases 1 to 138772)
             46753. .46938
/xpt_family="(TATATG\n"
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/rpt_family="CT-rich"
46753. .46938
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48559. .48780
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clone="P0518HC2"
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1 (bases 1 to 1182)

Yang, L., Wiegmann, B.M., Yeates, D.K. and Irwin, M.E.
Higher-level phylogeny of the Therevidae (Diptera: insecta) based on 28S ribosomal and elongation factor-1 alpha gene sequences
Mol. Phylogenet. Evol. 15 (3), 440-451 (2000)
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Stemogephrya sp. 288 ribosomal RNA gene, partial sequence.
AF147831
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Submitted (03-WAY-1999) Entomology, North Carolina State University, Box 7613, Raleigh, NC 27695, USA
Location/Qualifiers
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Pred. No. 5.6;
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16.3%; Score 38.8; DB 2; Length 16
Best Local Similarity 51.1%; Pred. No. 5.6;
Matches 91; Conservative 0; Mismatches 87; Indels
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/note="assembly_name:Contig16"
40638. .53634
1. .1984
/note="assembly_name:Contiglo"
2085. .4163
/note="assembly_name:Contigl1"
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/note="assembly_name:Contig14"
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Stenogephrya sp.
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                                                                                                                                             Direct Submission
Submitted (03-SEP-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63109, USA
Manmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 161010)
MCPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exercises of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: plasmid; 100$
Chemistry: Dye-primer ET; 0$ of reads
Chemistry: Dye-primer ET; 0$ of reads
Assembly program: Phrap; version 0.990119
Consensus quality: 157791 bases at least 040
Consensus quality: 157791 bases at least 020
Consensus quality: 155407 bases at least 020
Insert size: 17520; agarose-fp
Insert size: 15990; sum-of-contigs
Quality coverage: 10.01 in 020 bases; agarose-fp
Quality coverage: 10.14 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                   Center: Washirgton University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of unknown length
conting of 12997 bp in length
gap of unknown length
conting of 14844 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1984: contig of 1584 bp in length 2084: gap of unknown length 4263: contig of 2079 bp in length 4263: gap of unknown length 9331: contig of 5068 bp in length 16764: contig of 7338 bp in length 16764: gap of unknown length 21118: contig of 4254 bp in length 3095: contig of 4854 bp in length 31095: gap of unknown length 31095: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89216: contig of 20538 bp in length
89316: gap of unknown length
108734: contig of 19418 bp in length
108834: gap of unknown length
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of 10342 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                     ------ Summary Statistics ------
                                                                                                                                                                                                                                                                                        Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                        ---- Project Information -
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/organism="Mus musculus"
/mol_type="genomic DNA"
                                                                                                      2 (bases 1 to 161010)
McPherson, J.D. and Waterston, R.B.
                                                                                                                                                                                                                                                                                                                                                          Center project name: M BB0149E13
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/clone="RP24-149313"
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Sequencing vector: plasmid, n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 132361 bases at least Q40 Consensus quality: 132381 bases at least Q30 Consensus quality: 132389 bases at least Q20 Insert size: 134000; agarose-fp Insert size: 134000; agarose-fp Quality coverage: 11.10x in Q20 bases; agarose-fp Quality coverage: 11.10x in Q20 bases; sum-of-contigs
the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated
                                                                                                     with a Phrap-derived quality score.
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                                                                                                                                                                                                                                                                                           94 GAIGITCICGAAAAGGACTICCCAAAGTIATTGGAGTACTGTGAAAGAGTTCGTCATGAA 153
                                                                                                                                                                                                                                                                                                                                                                                                284 GAAATITIATAGAATTATTITITAATAGTTITIATATTAAAGTAATTGAATTIGGTAAGAG
                                                                                                                                                                                                                                           34 GAIGCAACAGICTICTCTCCAATIGGCAACTGTCTAJIAICCAITCCGCAATCACAITICG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae; Felis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (26-JAN-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 132389)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 GITTACCCAAAGGACTITACTATGTSAAFTAAATTGTCAAACTAGTAGTGTGGA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344 remecaerreagerarearecaarreaggaearreecaggrieggagriea 396
                                                                                                                                                                                           0;
                                                                                                                                        Length 1182;
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Pelis catus clone RP86-44312, WORKING DRAFT SEQUENCE.
AC108190
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                                                                                                                                             Score 38.6; DB 3;
Pred. No. 9.7;
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                /db_xref="taxon:95105"
<1. .>1182
/product="28S ribosomal RNA"
                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC108190.2 GI:25101059
HTG; HTGS_PHASE2; HTGS_DRAFT.
Felis catus (cat)
Felis catus
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l Similarity 51.4%;
89; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 CCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="clone overlaps with GenBank Accession Number AC108196 clone RP86-591N22 (center project name coc)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129445. .132389
/note="clone overlaps with GenBank Accession Number
AC108899 clone RP86-261015 (center project name cof)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70580. 132389
/note="clone overlaps with GenBank Accession Number
AC108193 clone RP86-469M8 (center project name coe)"
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* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 ATGTGAATTAAATTGTCAAACTAGTAGTCAGATCAATAAAATTCTACGTGGCA 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .132389
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                              /organism="Felis catus"
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/db_xref="taxon:9685"
/clone="RP86-44312"
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                                                                                                                                                                                                                                                                              Location/Qualifiers
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition,

Center clone name: 443102 Center project name: cod

AF071362 AF071362 B1175173 OSTR010H5 CB396206 OSTR168D4 AU115788 AU115788

BI175173 CB396206 AU115788 T01925

T01925 wEST02646 E
CB396141 CSTR167C8
CB39715 CSTR193H1
CB397765 CSTR193H1
CB37775 CSTR193H1
CB377765 CSTR193H2
CE71753 tigr-gss-CE71753 tigr-gss-CE71753 tigr-gss-CE745768 Fcylcold4
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CE444694 684795 MA
CF587970 USDA-FP_1

CE051398 CE717539 CF245758 AQ862746 CB444053 CF587970 BX353711

28

CB396141 CB396151 CB397715 CB397765

USDA-FP_1 BX353711

BX353711 BX553711
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BX015157 RCH223-3
BX569552 BX569552
C9431533 607523 MA
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BX186791 C850.2
C7440904 BST677249
C8393253 05TR11683
BX186791 C32 K 23BX623737 T3 EMG of

AZ512342 BZ8767139 BZ876771 AZ015157 AZ015157 CB431533 CB431633 CC939587 BY302654 BY302654 BY302654 BY302654 BY302654 BY302654 BY302654 BY302654 BY303794 CC740004 CC750004 CC750

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EQG02354 MI-P-HO-a BM537674 ha65c01.g AA532321 CpEST.451 BH312146 CH310-101 BX676706 BX676706 BH979578 Odf92908.

ALIGNMENTS

BH312146 BX676706 BH979578

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       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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AF071356 MRNA from cadmium-responsive gene Caenorhabditis elegans CDNA clone DDRT16, mRNA sequence. 1 (bases 1 to 238)

Liao, V.H.-C. and Freedman, J.H.
Cadmium-regulated genes from the nematode Caenorhabditis elegans.
Identification and cloning of new cadmium-responsive genes by
differential display
J. Biol. Chem. 273 (48), 31962-31970 (1998) Caenorhabditis elegans Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis. Nicholas School of the Environment Duke University Box 90328, Durham, NC 27708-0328, USA Email: jonf@duke.edu. Location/Qualifiers Contact: Jonathan H. Freedman AF071356 AF071356.1 GI:3265101 Caenorhabditis elegans 9822667 REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED FEATURES

source

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238 933 238 217

100.0 96.7 93.8 67.3

238 230.2 223.2 160.2

Description

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% Query Match Length DB

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SUMMARIES

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J. Biol. Chem. 273 (48), 31962-31970 (1998)
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Pred. No. 4.2e-42;
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Nicholas School of the Environment
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Location/Qualifiers
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J. Biol. Chem. 273 [48], 31962-31970 [1998]
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 933)
Liao, V.H.-C. and Freedman, J.H.
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                        /moi_type="mRNA"
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100.0%; Pred. No. 1.5e-45;
tive 0; Mismatches 0;
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Nicholas School of the Environment
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Matches 232, Conservative
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238 bp mRNA linear EST 25-NOV-1998 AF071379 mRNA from cadmium-responsive gene Caenorhabditis elegans AP071379 ö 61 ACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGACTTCCCAAAG 120 123 TTATTGGAGTACTGTGAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGA 182 63 ACTGICTATIATCCAITCCGCAATCACATTTCGGATGITCTCGAAAAGGACTTCCCAAAG 122 TTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGA 180 183 1 TITITITITITITIGGGAGGAAATCACGGCGGCGGATGCAACAGTCTTCTCTCAATTGGCA 60 62 GICTATIAICCATICCGCAATCACATITCGGAIGITCTCGAAAAGGACTICCCAAAGITA 123 1 (bases I to 218)
Liao,V.H.-C. and Freedman,J.H.
Cadmium-regulated genes from the nematode Caenorhabditis elegans.
Identification, and cloning of new cadmium-responsive genes by 3 TITITITITITITIGGGGAGGAATCACGGCTTCGGATGCAACAGTCTTCTCTCAATTGGCA 181 ATTAAATTGTCAAACTAGTAGTCAGTCAATAAAATTCTACGTGGCAAAAAAA 236 124 ITGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGAATT Gaps .. /tissue_type="whole animal" /dev stage="mixed population" /clone_lib="mRNA from cadmium-responsive gene" Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. Length 238; Indels

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Cadmium-regulated genes from the nematode Caenorhabditis elegans. Identification and cloning of new cadmium-responsive genes by differential display
J. Biol. Chem. 273 (48), 31962-31970 (1998)
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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/clone lib="mRNA from cadmium-responsive gene"
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Pred. No. 4.6e-27;
0; Mismatches 5;
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                                                                                                                                                                                                                                                          Box 90328, Durham, NC 27708-0328, USA Email: jonf@duke.edu.
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Dana Farber Cancer Institute
Street, Boston, MA 02115,
Tel: 617 632 5180
Fax: 617 632 2425
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Duke University
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                                                                                            APC71398 mRNA from cadmium-responsive gene Caenorhabditis elegans cDNA close DDXT7, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 ACTGICTAI -- AICAIICCGCAAICACAIIICGGAAGGTCTCGAAAAGG-CAIICCAAAG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TIATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGA 180
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                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 217)
Liao,V.H.-C. and Freedman,J.H.
Cadmium-regulated geres from the nematode Caenorhabditis elegans.
Identification and cloning of new cadmium-responsive genes by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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/dev_stāge="mixed population"
/clone_lib="mRNA from cadmium-responsive gene"
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.3%; Score 160.2; DB 9; Length 217; 92.2%; Pred. No. 2.4e-27; ive 0; Mismatches 13; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 ATTAAATTGTCAAACTAGTAGTCAGATCAATAAAATTCT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 ATTABATTGTCAAACTAGTAGTCGAGATCAATAAAATTTT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         differential display
J. Biol. Chem. 273 (48), 31962-31970 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Caenorhabditis elegans"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Jonathan H. Freedman
Nicholas School of the Environment
Duke University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Box 90328, Durham, NC 27708-0328,
Email: jonf@duke.edu.
Location/Qualifiers
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Liao, V.H.-C. and Freedman, J.H.
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|clone="DDRT7"
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EST 19-0CT-2000
                                                                                                                                                           /www.merm.composite and male"
/tissue_type="whole animal"
/dev.stage="mixed stage"
/dev.stage="mixed stage"
/clone lib="AD-wrmcDNA library was generated with poly(A)+
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 GICTATIAICCATICCGCAAICACATITCGGAIGTICTCGAAAAGGACTICCCAAAGTIA 123
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Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 ITTITITITIGGSAGGAAAICACGGCGGCGGAIGCAACAGICTICICICAAITGGCAACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 bp _RNA linear EST 19-0C1
AU115788 unpublished oligo-capped cDNA library Caenorhabditis
elegans CDNA clone yk736g5 3', mRNA sequence.
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/clone_lib="unpublished oligo-capped cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 TIGGAGTACTGTGAAAGAGTICGTCATGAAGTTTACCCAAAGGACTTTACT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 CTACAGTACTGTGAAAGAATCCGAAAGGAAATTTATCCAAATGATTTTACT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida;
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                38.2%; Score 91; DB 14; Length 583; 70.8%; Pred. No. 2.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Contact: Yuji Kohara
                                                                /organism="Caenorhabditis elegans"
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
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                                                                                        /mol_type="mRNA"
/strain="N2"
/db xref="taxon:6239"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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/strain="W2"
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Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 121; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CB396206 583 bp mRNA linear EST 15-WAY-2003 OSTR168D4_1 AD-wrmcDNA Caerorhabditis elegans CDNA, mRNA sequence.
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Seboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M.,
Armstrong, C.M., Li, S., Jacotoc, L., Bertin, N., Janky, R., Moore, T.,
Hudson, J. R., Harlley, J.L., Brasch, M.A., Vandenhaute, J., Boulcon, S.,
Endress, G.A., Jenna, S., Chever, E., Papasotiropoulos, V.,
Tolias, P.P., Pracek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFcome version 1.1: experimental verification of the
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
                                                                                                                                                                                                                                                                                                                                                       /dev_stage="mixed stage" /dev_stage="mixed stage" /dev_stage="mixed stage" /dlone_lib="mix-vrncoNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The DNAs were cloned into pPC86"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 GICIATTAICCATTCCGCAAICACATTTCGGAIGTTCTCGAAAAGGACTTCCCAAAGTTA 123
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Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans O cloning project : Contact jerome_reboul@dfci.harvard.edu or philippe_vaglio@dfci.harvard.edu
POLYA=No.
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 511;
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                                                                                                                                                                                                   'organism="Caenorhabditis elegans"
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Pred. No. 9.1e-20;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                    /sex="Hermaphrodite and male"
/tissue_type="whole animal"
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                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="N2"
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Marc Vidal Laboratory
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90.1%;
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Fax: 617 632 5739
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Best Local Similarity
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EST 15-MAY-2003
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Fax: 617 632 5180
Fax: 617 632 5739
Email: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
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                                                                        CB396141 567 bp mRNA linear EST 15-MAY-200 OSTRIFICE 1 AD-wrmcDNA Caenorhabditis elegans CDNA, mRNA sequence.
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Bukaryota; Metazoa; Nematoda; Chromadorea; Khabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Pred. No. 2e-08;
); Mismatches 41; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nat. Genet. (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
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/mol_type="mRNA"
/strain="N2"
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/tissue_type="whole animal"
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marc_vidal@dfci.harvard.edu
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                                                                                                                                                                                       Caenorhabditis elegans
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71.5%;
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                                                                                                                             IGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTTCCCAAAGTT 122
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                                                                                                                                                                                                               123 ATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTT-TACCCAAAGGACTTTACTATGTGAA 181
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MCCombie, W.R., Kelley, J.M., Aubin, L., Goscoechea, M.,
MitzGerald, M.G., Wu, A., Adams, M.D., Dubnick, M., Keriavage, A.R.,
Vencer, J.C. and Pields, C.A.
Caenorhabditis elegans CDNAs
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                                            190 TITCCIGITCGGAGACAAGATCACACCGGGGATGCAACAGTGTTTGGTCAATTGGCAAC
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Gaps
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/clone="CEDSX27"
/clone_lib="Early embryo, Stratagene (cat. #937007)"
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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9712 Medical Center Drive, Rockville, MD 20850 USA
    Indels
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    54;
    Mismatches
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Email: arkerlav@tigr.org
      ó
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Caenorhabditis elegans
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Contact: Kerlavage, AR
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      132; Conservative
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      Matches
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
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Gaps

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                                                                                                                                                                                                                                                                                               63 TGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTTCCCAAAGTT 122
                                                                                                                                                                                                                                                                                                                        123 ATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGAAT 182
                                                                                                                                                                                                                     3 TITITITITIGGAGGAGAAATCACGGCGGGAGCGAACAGTCTTCTCTCAATTGGCAAC 62
                                                                                                                                                                                                                                                                                                                                                                                                       116 ILCTAACHACHTATAACHGCATGACHGACHGATAAAGGCAGTTATHAAAGTCT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                183 TARATIGICARACTAGTAGTCAGATCAATARAATTCTACGTGSCARARARARA 238
                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mcl_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="texon:9615"
/Tofe lib="bog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
                                                                                                                                            Query Match 17.1%; Score 40.8; DB 29; Length 636; Best Local Similarity 48.3%; Pred. No. 12; Matches 114; Conservative 0; Mismatches 122; Indels 0.
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Search completed: July 7, 2004, 16:21:39 Job time: 2513 secs

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7, 2004, 11:39:02; Search time 349 Seconds (without alignments) 2897.052 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                        3373863 seqs, 2124099041 residues
                                                                         OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STRANSPIRS

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		40				
Result No.	Score	Query	Query Match Length DB	DB	£	Description
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1					
М	34.6	14.5	199	Ŋ	ABV55254	Abv55254 Human pro
0	34.6	14.5	6036	ø	ABN80125	Abn80125 Human che
m	33.6	14.1	671	m	AAA27331	Aaa27331 Soybean p
~t*	33.4	14.0	404	æ	ACH29861	Ach29861 Human tes
ο σ	33.4	14.0	1208	4	AAD16067	Aad16067 Soybean z
υ Q	33.2	13.9	8781	9	ABL33686	Abl33686 Human imm
c, 7	33	13.9	20693	4	ABL16740	Abl16740 Drosophil
ω υ	32.8	13.8	571	ف	ABX09781	Abx09781 M. incogn
0	32.8	13.8	678	ω	ABQ65781	Abq65781 Arabidops
c 30	32.8	13.8		4	AAK87745	Aak87745 Human dig
0 11	32.8	13.8		4	AAI57549	Aais7549 Human col
c 12	32.8	13.8	745	ψ	ABS99726	Abs99726 cDNA enco
c 13	32.8	13.8	745	σ	ADB92806	Adb92806 Human col
14	32.8	13.8	2630	4	ABL29872	Abl29872 Drosophil
15	32.8	13.8	3423	φ	ABQ70819	Abg70819 Listeria
26	32.8	13.8		4	ABL02096	Abl02096 Drosophil
17				4	ABL29758	Abl29758 Drosophil
C 18		13.8	αņ	9	ABQ67094	Abg67094 Human ang
e i		_		9	ABL58167	Abl58167 Human glu
c 20	32.6	_	6117	ø	ABL34490	Abl34490 Human met
c 21		13	6561	9	ABN80020	Abn80020 Human che
c 22	32.6	13.7	37184	9	ABQ67077	Abq67077 Human ang
23	32.4	13.6	675	œ	AAL57561	Aal57561 Human mag

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing

Aaa76188 Swine inf		Adb54264 Pretreate	Abl32467 Human imm	Continuation (5 of		Aat91324 Arabidops		Abz16757 Arabidops	Abl40935 Human nuc		Abk31326 Signal tr	Ada03023 Mouse Mbn	Adb72761 Mouse Mbn	Adc85503 Mouse Mbn	Continuation (4 of	Aaa45239 Human sec	Aah33523 Human col	Aai94027 Human neu	Aaa74870 Murine ch	Aav04063 Schizosac	Abn83979 Human gen	
AAA76188	ABL29304	ADB54264	ABL32467	ABA90521 04	ABT07607	AAT91324	AA196712	ABZ16757	AB140935	AAS46465	ABK31326	ADA03023	ADB72761	ADC85503	ACH03408 3	AAA45239	AAH33523	AAI94027	AAA74870	AAV04063	ABN83979	
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13.6	13.6	13.6	13.5	13.5	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.3	13.3	13.3	13.3	13.3	13.3	
32.4	32.4	32.4	32.2	32.2	32	32	31.8	31.8	31.8	31.8	31.8	31.8	31.8	31.8	31.8	31.6	31,6	31.6	31.6	31.6	31.6	1
24	25	26	27	28	29	30	33	32	33	34	35	36	3,7	38	39	40	4.1	42	43	44	7.)
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ALIGNMENTS

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Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
                                                                                       Human prostate expression marker cDMA 55245.
                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 10673; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                 Monahan JE;
                     ABV55254 standard; cDNA; 199 BP
                                                                                                                                                                                                                                          17-FEB-2000; 2000US-0183319P.
16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0207454P.
09-UJN-2000; 2000US-0211314P.
18-UJL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-025281P.
                                                                                                                                                                                                                      20-FEB-2001; 2001WO-US005171.
                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-662795/76.
                                                                                                                                                                          W0200160860-A2.
                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                 23-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                    Schlegel R,
                                                                  17-SEP-2002
                                            ABV55254;
RESULT 1
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Indels

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Matches

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Query Match

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3831 reaaarratrecectraatraraaaacaaaaraaaraaaraaarreaaarreceedaaara 3772
Oligomers specific to each of the genes are useful for detecting the methylation state of all CpG dinucleotides within the 350 sequences or [11) and their complementary sequences, as primer oligonucleotides for the amplification of the 350 sequences, [17] and/or their complements and as oligomer probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs). Note: The sequence data for this patent did not form part of the printed specification but is based on begennce information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glutamine amidotransferase; histidine biosynthesis; herbicide; fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotides encoding plant glutamine amidotransferase homologs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a Glycine max (soybean) putative glutamine amidotransferase coding sequence. The protein forms a crucial stage in
                                                                                                                                                                                                                                                                                                                                                       110 ACTICCCAAAGITAITGGAGIACTGIGAAAGAGITCGICATGAAGITIACCCAAAGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 TIACTATGIGAATTAAATTGICAAACTAGTAGTCAGATCAATAAAATTCTACGTGGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for producing transgenic plants and as probes or primers
                                                                                                                                                                                                                                                            Score 34.6; DB 6; Length 6036; Pred. No. 6.4;
                                                                                                                                                                                                                Sequence 6036 BP; 1473 A; 98 C; 1516 G; 2949 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "glutamine amidotransferase"
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/transl_except= {pos
/note= "Xaa=unknown"
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                                                                                                                                                                                                                                                               14.5%;
54.3%;
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Best Local Similarity 54.34;
Since 70; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-376564/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    development genes, in particular disease related to homeobox containing genes (HCX) like diabetes, cancer, apoptosis related diseases, syndromes associated with congenital heart disease, epilepsy, diseases related to histone deacetylation, Currarino syndrome, diseases related with the development of the brain and limb girdle muscular dystrophy and dwarfism.
       the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient
                                                                                                                                                                                                                                                                                                                     150 TGAAGTTTACCCAAAGGACTTTACTATGTGAATTAAATTGTCAAACTAGTAGTCAGATCA 209
                                                                                                                                                                                                                                                                                                                                                              57 TGCAGGATACACAATTGACACAAAAAGGAAAATAATAAAGTCAAACTGGTATTCAAAAA 116
                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Furnan, development; homeobox gene; HOX; diabetes; cancer; apoptosis;
teart cisease; epilepsy; histone deacetylation; ruscular dystrophy;
dwarfism; single nuclectide polymorphism; SNP; cytosine methylation;
antidiabetic; cytosettic; anticorvulsant; ds.
                                                                                                                                  is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sec of a segment of chemically pretreated DNA of genes associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human chemically modified disease associated gene SEQ ID NO 142.
                                                                                                                                                                                                                       Length 199;
                                                                                                                                                                                                                                                                         34; Indels
                                                                                                                                                                              Sequence 199 3P; 105 A; 34 C; 37 G; 22 T; 0 U; 1 Other;
                                                                                                                                                                                                                            DB 5;
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Pred. No. 2.2;
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61.8%;
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                                                                                                                                                                                                                                                     Local Similarity
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Homo sapiens.

Synthetic.

15-JUL-2002

ABN80125;

30-JUN-2000; 01-SEP-2000;

ABNOLL 2
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ABNOLL 3
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03-JAN-2002

development.

105

2;

91; DB 8;

Length 404; Indels

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for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated CDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was sequated in electronic format directly from USPTO at sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                     161 ingrisianaingacagagcicirinahaachaagcaamiraahirintighachagaa 220
                                                                                                                                                                                                                                                                                                                                                                                                                                          106 AAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 AAAATTTGAACATTTTÄGTTCTTGGTTATAAAATGTTAATTCAGAA--TTÄGTTTÄÄT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACTITACTATGARITAAATTGTCAAACTAGTAGTCAGATCAATAAAATTCTACGTGG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 GCCTTAATTAAACTAATTAATAGCTTTGGACACTTAAAAGAGCTCTAAATTTGCTTGTAA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New arsenic transporter polypeptides and polynucleotides, useful for producing transgenic plants with altered level of heavy metal tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transporter; zinc transporter; transgenic plant; soybean;
                                                                                                                                                                                                                                                                                                                                             46 TICTCTCAATTGGCAACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soybean zinc transporter (ZnT-2) cDNA from clone se6.pk0012.h2:fis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    t= "Soybean zinc transporter protein" "CDS does not include start codon"
                                                                                                                                                                                                  Sequence 404 BP; 143 A; 43 C; 77 G; 137 T; 0 U; 4 Other;
                                                                                                                                                                                                                                             14.0%; Score 33.4; DB
51.8%; Pred. No. 6.3;
:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sakai H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00461474.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Eirst entry)
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                                                                                                                                                                                                                                                                              Best Local Similarity 51.8
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Allen SM, Rafalski JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 CAAAAAAAAAAA
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P-PSDB; AAE09323.
                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-DEC-1998;
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                                                                                                                                                                                                                                                     Query Match
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  the histidine biosynthesis pathway. The sequence can be used to create transgenic plants which express different amounts of the protein, to identify loss of function mutants and to produce the protein in a host cell, for example a bacterium. The protein can be used to identify inhibitors which may be useful as functioned and herbicides. The gene was identified by computer screening for sequences which could encode
                                                                                                                                                                                                                                                                                                                                                     143 TICGICALGAAGITTACCCAAAGGACTTTACTATGIGAATTAAATTGTCAAACTAGTAGT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, ss, sequencing by hybridisation, SBH, expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA libraries, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          one of
                                                                                                                                                                                                                                                                                                                                                                                                  572 Trichaharmitriaaccaaaarmitraccarciiccaccarriccacarriici 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated polynucleotide comprising any one of 18543 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide sequences obtained from various cDNA libraries, usef as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                       DB 3; Length 671;
                                                                                                                                                                                                          Sequence 671 BP; 217 A; 104 C; 144 G; 205 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 CAGATCAATAAAATTCTACGTGGCAAAAAAAAAAA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  632 TATTACAAATTATTTCATGTGTCAAAAAAAAAA 667
                                                                                                                                                                                                                                                       Score 33.6; Di
Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 17073; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stache-Crain B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACH29861 standard; cDNA; 404 BP
                                                                                                                                                          histidine biosynthetic enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                          14.1%;
59.4%;
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                                                                                                                                                                                                                                                                                                          57; Conservative
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) STACHE-CRAIN B.
// DICKSON M C.
TONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human testis cDNA #247.
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                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                          Query Match
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53; DB 6;

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Length 8781;

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121 TIATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGA 180
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provides a number of human immune system associated
    The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, ansemia, cancer, acute myeloid teletaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, richumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genomic polynucleotide SEQ ID NO 1693.
                                                                                                                                                                                                           Sequence 8781 BP; 2407 A; 65 C; 2093 G; 4216 T; 0 U; 0 Other;
                                                                                                                                                                                                                                      Score 33.2; DB
                                                                                                                                                                                                                                                                                  Pred. No. 19;
0; Mismatches
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                                                                                                                                                                                                                                                              13.9%;
55.1%;
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                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                             65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL16740;
                                                                                                                                                                                                                                                                                                                                                                                                       191
                                                                                                                                                                                                                                                                 Query Match
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         The invention relates to heavy metal (e.g. arsemite and zinc) transporter polypeptides and polymeideotides. The polypeptides of the invention are useful for producing antibodies that are useful for screening CDNA expression libraries to isolate full length clones of interest. The antibodies are also useful for detecting the polypeptides in situ, in cells or in vitro, in cell extracts. Nucleic acid molecules of the invention are useful for producing transgeric plants with altered tolerance to the neary metals. They are also useful as probes for genetically and physically mapping the genes that are a part of, and as markers for traits linked to those genes. The present sequence is soybean zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              802
                                                                                                                                                                                                                                                                                                                                                                                                                                  CAATTGGCAACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGAC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            804 Triccada Arginic de de Genera de Terres de Contra Cara de 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, immune system disease, cytosine methylation, antiasthmatic; antiatioscleroitic, antiamednic; cytostatic; nootropic; neuropic; neuropic; anti-HV, anticonvulsant, ophthalmologic; anti-HV, anticonvulsant, ophthalmological; antirhermatic; antiathritis, antidiabetic; antipsoriatic; antiathritis, antidiabetic; artisociatic; antinifammatory; cancer; eye disease; arcerlosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; ALDS; epilepsy; neurofibromatosis; rhenmatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              864 CAACAGCCCCCTTTCAAGCTTAGTAGCATCTATCTCACGAGGTGTGTTCTCCATCAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 TICCCAAAGTIAITIGGAGIACIGIGAAAGAGTICGICAIGAAGITIACCCAAAGGACTIT
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
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                                                                                                                                                                                                                                                                                            Sequence 1208 BP; 347 A; 208 C; 281 G; 372 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune system associated gene SEQ ID NO: 1659.
                                                                                                                                                                                                                                                                                                                                                                                      56;
                                                                                                                                                                                                                                                                                                                                        Score 33.4; Dl
Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                transporter (ZnT-2) protein cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL33686 standard; DNA; 8781 BP.
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2000DB-01043826.
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                                                                                                                                                                                                                                                                                                                                          14.0%;
54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                         , 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL33686;
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Best Local 8
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ABL33686/C
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG175-ABLIG17), expressed DNA sequences (ABLIG175) and the encoded proteins (ABB77773-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20693 BP; 6230 A; 4195 C; 3675 G; 6543 T; 0 U; 0 Other;
                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1693; 21pp + Sequence Listing; English.
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163 AAGGACTTTACTATGTGAATTAAATTGTCAAACTAGTAGTCAGATCAATAAAATTCTACG 222
                                                                                                                                                                                                                                                                                                                                                                                                  82 AAGGAATTAAAATGTGTTAAATTGTTAAATGATTTTTCTGAGTAAATTTATTGTTGA 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana; thale cress; plant; transgenic; GMO; disease; stress; metabolic pathway; biosynthetic pathway; nutrition; fungicide; insecticide; antibiotic; ds.
produce nematode inhibitors or RNAi in the plants, and provide new biorechnological strategies for managing nematodes under sustainable agricultural conditions. ABX09677-ABX09815 represent RNAi molecules useful for the control of nematodes
                                                                                                                                                                                                                    DB 6; Length 571;
                                                                                                                                                          Sequence 571 BP; 151 A; 142 C; 72 G; 205 T; 0 J; 1 Other;
                                                                                                                                                                                                                                                                              27; Indels
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Ledford BL, Woessner
, Davis KR, Allen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana polynucleotide SEQ ID NO 358.
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                                                                                                                                                                                                                 13.8%; Score 32.8; 64.5%; Pred. No. 10
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Page A, Mathew AV,
Kricker M, Slater T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABQ65781 standard; DNA; 678 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 TGGCAAAAAAAAA 238
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49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WOESSNER J P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAMEAKA J G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-479224/51.
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RAINES T M.
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MATHEW A V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GARCIA C A.
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DAVIS K R.
ALLEN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOFFMAN N.
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Best Local S
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(ALLE/)
(HOFF/)
(HURB/)
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(PRIC/)
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(PAGE/)
(MATH/)
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                                                                                                                                                                                              11638 ATTTCCAATGATTATCCTTTGATACGTATTCACCTTTTGGTGTTTTCCCATATGTATAT 11579
                                                                                                                                                                                                                                                                                                                     11578 TCCAAATACATTTCAATTGGTCCTCAAAGTGGTTCGGTAATATCCCCAAATATGCATTAC 11519
                                                                          Ö
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                                                                                                                                    113
                                                                                                                                                                                                                                                        114 CCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTAC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to RNAi (double-stranded interfering RNA or
                                                                                                                                                                                                                                                                                                                                                                                                                                  11518 CATCACCALTITAAATGAATACTACTTGTCCGGAAACACAAACGTTAGATGGTCAAA 11462
                                                                                                                                                                                                                                                                                                                                                                                     174 TATGTGAATTAAATTGTCAAACTAGTAGTCAGATCAATAAAATTCTACGTGGCAAAA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA mediated interference; mRNA transcript, nematode gene; growth; development; parasitism; reproduction; RNAi vector; mRNA translation; nematode inhibitor; agricultural industry; anti-nematode; ds.
                                                                                                                             54 ATTGGCAACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTT
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA; molecule; double-stranded interfering RNA; nematode control;
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            DB 4; Length 20693;
28;
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                                                                          Indels
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                                                                          90;
            Score 33; DB 4, Pred. No. 28; 0; Mismatches
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                13.9%;
49.2%;
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Matches
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Haas WD;

JP, Haas | Hoffman N;

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2000US-C246477P.
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2000US-0225270P.
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        14-AUG-2000; 2
14-AUG-2000; 2
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01-SEP-2000; 2
05-SEP-2000; 2
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20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
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22-AUG-2900;
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06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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12-SEP-2000;
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25-SEP-2000;
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27-SEP-2000;
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The invention relates to nucleic acids (1) that hybridise under stringent conditions to any of 999 sequences (ABQ6542-ABQ66422) or their fragments. (1) are used to express the corresponding polyperides (II) or to produce genetically modified plant cells or transgenic plants, which may have improved resistance to disease or stress, or altered metabolic/blosynthetic pathways (for production of commercial, nutritional or medicinal products), or generally any trait of interest, or can be used to screen for biologically active agents (e.g. fungicides, insecticides and antibiotics). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in sequence constant directly from the USPTO at
                                                                                                                                                                                                                                                               163 AAGGACTTTACTATGTGAATTAAATTGTCAAACTAGTRGTCAGATCAATAAATTCTACG 222
                                                                                                                                                                                                                                                                                   83 ATGTAATGTTTTATGTGGGTTTGAGTTGTAATACTTGCTTTTGCATAAAAATGGTTTG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, digestive system antigen, gene therapy, cancer, appendicitis, ulcerative colitis, infection, Hirschsprung's disease, chronic colitis, digestive system disorder, Meckel's diverticulum; ss.
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Auman digestive system antigen coding sequence SEQ ID NO: 61.
                                                                                                                                                                                                                 Score 32.8; DB 6; Length 678;
Pred. No. 11;
                                                                                                                                                                                            Segrence 678 BP; 161 A; 198 C; 110 G; 209 T; 0 U; 0 Other;
                                                                                                                                                                                                                                        27; Indels
                      Claim 1; SEQ ID NO 358; 40pp + Sequence Listing; English
                                                                                                                                                                                                                 Match 13.8%; Score 32.8; Di Local Similarity 64.5%; Pred. No. 11; es 49; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          AAK87745 standard; cDNA; 745 BP.
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18-ARR-2000; 2000US-019121P.
19-MAY-2000; 2000US-0209467P.
07-UUN-2000; 2000US-0209467P.
28-UUN-2000; 2000US-021488FP.
07-UUN-2009; 2000US-021518FP.
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2000US-0184664P.
2000US-0186350P.
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  altered metabolism.
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02-MAR-2000;
16-MAR-2000;
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04-FEB-2000;
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AGATGATITIAGGGACATITIATITITAAATITACAATCTAATGGTNANAAAAAA 49
                                                                                                                                                                                                                                            Human; colorectal cancer; colorectal cancer antigen; gene therapy; ss.
                                                                                                                                                                                                                   Human colorectal cancer antigen cDNA SEQ ID NO: 13.
                                         213 AAATTCTACGTGGCAAAAAAAAAA 238
                                                                 BP
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C1-SEP-2000; 2000US-022937P.
01-SEP-2000; 2000US-0229343P.
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2000US-0205515P.
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2000US-0220963P.
2000US-0220964P.
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2000US-0229509P.
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2000US-0230437P
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2000US-0231242P.
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                                                                                                                                                                                         (first entry)
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02-MAR-2000; 2
16-MAR-2000; 2
17-MAR-2000; 2
19-APR-2000; 2
19-MAY-2000; 2
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01-SEP-2000; 2
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30-JUN-2000;
07-JUL-2000;
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22-AUG-2000;
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ID AAI5
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2000US-0246609P.
2000US-0246610P.
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2000US-0249210P.
2000US-0249211P.
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2000US-0246613P.
2000US-0249207P.
2000US-0249208P.
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2000US-0250160P.
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2000US-0249213P.
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2000JS-0249215P.
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2000US-C246528P.
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Best Local Similarity
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05-JAN-2001;

08-NOV-2000 09-NOV-2000 09-NOV-2000 017-NOV-2000 017-NOV-2

Matches

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20-OCT-2000) 200035-0241803P.
20-OCT-2000) 2000035-0244817P.
C1-NOV-2000) 2000035-0244617P.
08-NOV-2000) 2000035-0246474F.
08-NOV-2000) 2000035-0246476F.
08-NOV-2000) 2000035-0246476F.
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08-NOV-2000, 2000US-0246610P.

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17-NOV-2000, 200US-0246611P.

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08-NOV-2000; 2000US-0246526P.
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2000US-0249214P.
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20-0CT-2000; 2000US-0241785P.
20-0CT-2000; 2000US-0241786P.
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                       08-SEP-2000; 2
08-SEP-2000; 2
08-SEP-2000; 2
12-SEP-2000; 2
14-SEP-2000; 2
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02-OCT-2000;
02-OCT-2000;
13-OCT-2000;
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17-NOV-2000;
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29-SEP-2000;
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20-OCT-2000;
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The present invention provides the protein and coding sequences of a number of colorectal cancer antigens. These are shown in AAL57547-AAL57619 and AAM38569-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen coding sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 AGTITACCCAAAGGACTTTACTATGTGAATTAAATTGTCAAACTAGTAGTCGGATCAATA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 AGATGATTTTAGGGACATTTTATTTTAAATTTACAATCTAATGGTNANAAAAAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, colorectal cancer related protein; colon; rectum; colorectal cancer metastasis; gastrointestinal disorder; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding human colorectal cancer related protein #3.
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ABS99726 standard; cDNA; 745 BP.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024939P.
17-NOV-2000; 2000US-024930P.
01-DEC-2000; 2000US-0250160P.
05-DEC-2000; 2000US-025198P.
05-DEC-2000; 2000US-02519P.
06-DEC-2000; 2000US-02519P.
06-DEC-2000; 2000US-02518FEP.
08-DEC-2000; 2000US-02518FEP.
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Best Local Similarity 60.5
Matches 52; Conservative
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P-PSDB; AAM38571.
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musculoskeletal system disorder; Albers-Schonberg disease;
Marfan's syndrome; neurological disease; phenylketonuria;
Mernicke's encephalogathy; Alzheimer's diseases; endocrine disorder;
Grave's disease; Cushing's syndrome; reproductive system disorder;
prostatosis; benign prostatic hypertrophy; benign prostatic hyperplasia;
thrombosis; atherosclerosis; myocardial infarction; ischaemic attack.
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2000US-0225759P
2000US-022681P
2000US-022688P
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2000US-022688P
2000US-0227182P
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2000US-0230438P.
2000US-0231242P.
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28-JUN-2000; 2000US-0214886P.
30-JUN-2000; 2000US-0215135P.
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2000US-0220964P.
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14-AUG-2000; 2000US-0224519P.
14-AUG-2000; 2000US-025213P.
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2000US-0225268P.
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2000US-0229287P.
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08-SEP-2000; 2000US-0231244P.
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17-MAR-2000; 2000US-0190076P
18-APR-2000; 2000US-0198123P
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07-JUL-2000;
11-JUL-2000;
                                                                                                                                        Homo sapiens.
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14-AUG-2000;
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         The present invention relates to the isolation of novel human colorectal cancer related proteins, and polymucleotide sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of the calon and/or rectum, including colorectal cancer, colorectal cancer metastases, and gastrointestical disorders such as dysphagia, peptic oesophagitis, gastric reflux, claritable bowel syndrome, and peritoneal diseases. The invention also describes antibodies that bind colorectal cancer related proteins, overcors, host cells, and recombinant and synthetic methods for producing human colorectal cancer related polynucleotides, polypeptides, and/or antibodies. ABS99796 represent colorectal cancer related processins. Note: The sequence encoding human colorectal cancer related processins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format diacetly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 AGITTACCCAAAGGACTTTACTATGTGAATTAAATTGTCAAAACTAGTGGTCAGATCAATA 212
                                                                                                                                                                                                                                                                                                          New colorectal cancer polypeptide for Giagnosing, prognosing, preventing, and treating immune, hyperproliferative, liver, kidney, reproductive disorders and for identifying modulators of therapeutic use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptic ulcer, Bruton's disease, X linked infantile agammaglobulinaemia, severe combined immunodeficiency; DiGeorge anomaly, hyperproliferative disorder; acute lymphoblastic leukaemia, acute lymphocytic leukaemia; urinary system disorder; cortical necrosis; kidney infarction; cardionscular disorder; carcinoid heart disease; arrinythmia; respiratory disorder; non-allergic rhinitis; simusitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 AGAIGATITIAGGGACATITITATITITAAATITAAATITIACAATCIAATGGINANAAAAAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      small intestine non-Hodgkin's lymphoma; small bowel lymphoma; ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ss; gene, human, cclorectal cancer, antigen; gene therapy; gastrointestinal disorder; inflammatory disease; infection; cancer; intestinal neoplasm; small intestine carcinoid tumour;
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                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; SEQ ID NO 13; 183pp; English
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                                                                17-JAN-2001; 2001US-00764855.
                                                                                                   31-JAN-2000; 2000US-0179065P
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                                                                                                                                                                                                                  Ruben SM,
                                                                                                                                                                                                                                                     WPI; 2002-731367/79.
                                                                                                                                      (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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01-DEC-2000; 20c0US-0250160P.
01-DEC-2000; 20c0US-0250391P.
05-DEC-2000; 20c0US-0251030P.
05-DEC-2000; 20c0US-025103P.
06-DEC-2000; 20c0US-025149P.
06-DEC-2000; 2000US-025149P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251868P.
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20-OCT-2000; 2000US-0241803P.
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20-OCT-2000; 2000US-0241803P.
20-OCT-2000; 2000US-024617P.
08-NOV-2000; 2000US-0246477P.
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08-NOV-2000; 2000US-0246478P.
08-NOV-2000; 2000US-0246478P.
08-NOV-2000; 2000US-024652P.
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The invention relates to a colorectal cancer antigen. The antigen is useful for chromosome identification, chromosome mapping, radiation by brid ampping or gene therapy, or as hybridisation probes for differential identification of the tissues or cell types present in a colorical sample. The antigen is useful for treating, preventing, inflammandory diseases and/or conditions, infections, cancers (e.g., inflammandory diseases and/or conditions, infections, cancers (e.g., intestinal neoplasms (carcinoid tumour of the small intestine, normal encetinal neoplasms (carcinoid tumour of the small intestine, normal officers; The antigen and its mucleic acid are useful cto provide immunological probes for differential identification of the immune system e.g. Bruton's diseases, disorders and/or conditions of the immune system e.g. Bruton's diseases, disorders and/or conditions of the immune system e.g. Bruton's diseases, X linked infantile agammaglobulinaemia, severe combined immunodeficiencies, Diceorge commanly, etc. The antigen and its nucleic acid is useful for treating, preventing and/or diagnosing hyperproliferative disorders (e.g. acute
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Pred. No. 11;
0; Mismatches 34; Indels (
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illarity 60.5%; Pre
Conservative 0;
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11-JUL-2000; 2000US-00614150.
08-DEC-2000; 2000US-0251989P-

08-DEC-2000; 2000US-0251990P-

11-DEC-2000; 2000US-025907P-

C5-JAN-2001; 2001US-0259678P-

17-JAN-2001; 2001US-02596785.
                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                 Ruben SM,
                                                                                                                                                                                    WPI; 2003-708345/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                     P-PSDB: ADB92879.
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                                                                                                                                                   Rosen CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB7737-ABB7072). The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 ATCACATITCGGATGITCTCGAAAAGGACTTCCCAAAGTTAITGGAGTACTGTGAAAGAG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         505 TAATGGCAGTTAAAGATGTTTGTCAAGTGGTGTCATTAAATTATATGTTATGT 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 TCACGGCGCGCGATGCAACAGTCTTCTCTCAATTGGCAACTGTCTATTATCCATTCCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 ITCGTCATGAAGTITACCCAAAGGACTITACTATGTGAATTAAATTGTCAAA 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.8%; Score 32.8; DB 4; Length 2630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2630 BP; 725 A; 579 C; 613 G; 713 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 41089; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0, Mismatches
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                                                                                                                        Myers BW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
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                                                                                                                        PWD,
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(first entry)
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(CNRS ) CNRS CENT NAT
                                                                                                                    Adams M,
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                                                                                                                                                                                              WPI; 2001-656860/75
                                     (PEKE ) PE CORP NY.
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29-AUG-2002
                                                                                                                        Wenter JC,
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113 A8Q7

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The present invention relates to nucleic acid sequences (ABG67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. and contaminants in foods, or mutational analysis) and for analysis of sexpression. Proteins encoded by the rucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in antifisteria vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at trp, wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2377 GAATTIGITITITATCTTTTCCCCAAGCACAAACGAATGGTATGGATGAAAACTTCGCT 2436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 GCAACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTTCCCA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
New gencric sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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59.8%; Pred. No. 18
                                                                                                                                                                             Claim 14; SEQ ID NO 3632; 180pp; French
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Sequence 11, Appli
Sequence 213, Appli
Sequence 213, Appli
Sequence 3, Appli
Sequence 38, Appli
Sequence 38, Appli
Sequence 49, Appl
Sequence 149, Appl
Sequence 149, Appli
Sequence 266, Appli
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Sequence 91, Appl
Sequence 93, Appl
Sequence 91, Appl
Sequence 2, Appli
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1, App
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1630.596 Million cell updates/sec
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Sequence 10, A
Sequence 99, A
Sequence 101,
Sequence 99, A
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                                                     July 7, 2004, 13:49:08; Search time 81 Seconds
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUB_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUB_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                    OM nucleic - nucleic search, using sw model
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seq length: 200000000
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   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in 14.0%; Score 33.4; DB 3; Length 1208; Similarity 54.5%; Pred. No. 0.56; 67; Conservative 0; Mismatches 56; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-09-197-679A-1
Sequence 1, Application US/09197679A
; Sequence 1, Application US/09197679A
; GENERAL INFORMATION:
    APPLICANT: Foley, Patricia L
    TITLE OF INVENTION: Vaccine Against Swine Influence
    NUMBER OF SEQUENCES: 2
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Hendricks and Associates
    STREET: P.O. Box 2509
US-08-459-324-2

US-09-107-5228-359-

US-08-413-608B-1

US-08-724-3948-20

US-08-724-3948-22

US-08-724-3948-22

US-08-724-3948-22

US-08-724-3948-22

US-09-444-316-6

US-09-444-316-6

US-09-135-406-1

US-09-135-406-1

US-09-135-406-1

US-09-135-406-1

US-09-135-406-1

US-09-134-0010-362

US-09-133-381-1759

US-09-888-9
                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION

GENERAL INFORMATION

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Allen, Steve

APPLICANT: Rafalski, Antoni

APPLICANT: Rafalski, Antoni

APPLICANT: BARAi, Hajime

TILE OF INVENTION: Plant Wetal Transporters

FILE REFERENCE: BB1303 US NA

CURRENT APPLICATION WINBER: 08/09/461,474

CURRENT APPLICATION NUMBER: 60/112,562

EARLIER FILING DATE: 1999-12-14

SERIIGN FILING DATE: 1999-12-16

SOFTWARE: Microsoft Office 97

SEQ ID NO: 11

SEQ ID NO: 11

SEQ ID NO: 11

SED IN NO: 11
                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                       2322
1830121
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2322
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2163
3338
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246240
246240
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Matches 67; Conserv
   172 ACT 174
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                                                                                                                                                                                                                                                                                                                                                                           US-09-461-474-11/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1208
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   28.8
28.6
28.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 ACTICCCAAAGITATIGGAGTACIGIGAAAGAGITCGICAIGAAGITTACCCAAAGGACT 169
                                                                                       175 MAWGKKWWRYATTWRRAMMWWAAWTMMWTWWWAWCMSSRGAAMYRRTMMMGYRYWWRK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 CTCAATTGGCAACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGG 109
235 IWCYNYWKYWKRMWSKICWSGSRGGYMISYISIRSYSMYWASWWKTMCWWWGRWWSIYWY 176
                                             67 TAT--TATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTTCCCAAAGTTAT 124
                                                                                                                                125 TGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGAATTA 184
                                                                                                                                                              115 KSYRRTRCAMAYAWKIKRSYYWCWRWKWKRCMMMMMAMAYGKINMMRACWKIRYWRWNA 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Davis, Roger J.
APPLICANT: Davis, Roger J.
APPLICANT: Galcheva-Gargova, Zoya
TITLE OF INVENTION: NON-ACTIVATED RECEPTOR COMPLEX
TITLE OF INVENTION: PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER TRADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: MINIOWS95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,513
FILING DATE: 06-UN-1997
PRICR APPLICATION DATA:
APPLICATION NUMBER: 060-UN-1997
FILING DATE: 060-UN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31.6; DE
Pred. No. 3.5;
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08870518; Patent No. 5925566; GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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617/542-8906
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 85; Conservat
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US-08-870-518-7
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                                                                                                                                                                                                                                                                                                                                                            US-08-870-518-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Indels
                                                                                                                                       COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1646 GCAATCAGTTTCTGGATGTGCTCCAATGGGTCTTTACA 1683
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APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPRENCE: GENSET 054 PR.2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILNO BATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent,pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32.4; DB 3;
Pred, No. 1.3;
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                                                                                                                                                                                                     CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/09/197,679A
FILING DATE: 23-No. 628/570-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30; Conservative 112; Mismatches
                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REFERENCE/DOCKET NUMBER: foley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2813, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-8405
TELEFAX: (703) 425-8406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1724 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 13.6%;
l Similarity 58.2%;
57; Conservative
                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                STATE: Virginia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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                                                                           ZIP: 22031
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Best Local Similarity
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Matches 30; Conserv
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US-09-621-976-2813/c
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170 ITACIAIGEGRAITAAAITGECAAACTAGEGGGGGGGTGAIGAAITGEAGG 223

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7 TETETITGGGAGGAAATCACGGCGGCAGGATGCAACAGTCTTCTCTCAATTGGCAACTGTC

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TITLE OF INVENTION: GENER ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE (PARG)
TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES INMUNORBACT
TITLE OF INVENTION: THEREMITH
FILE REPERENCE: NIAD 201
CURRENT APPLICATION NUMBER: US/09/511,477
PRIOR PRILICATION NUMBER: US/09/511,477
PRIOR APPLICATION NUMBER: US/09/302,812
PRIOR FILING DATE: 1999-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21128 TİTİTÜÇÜĞATTAAAĞIĞAATİCAAARITİTTATIĞIĞATATGÜLÜĞİTÜTAĞTAAATT 21069
                                                                                                                                                                                                                                                                                                                                                                                                        21128 Trirircicarnaaagrigaarricaaaararrirrarrickararscriggrichagraarr 21069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 GATGTTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 GITTACCCAAAGGACTITACTAIGIGAATTAAAIIGICAAACTAGTAGTCAGAICAATAA 213
                                                                                                                                                                                                                                                94 GAIGITCICGAAAAGGACTICCCAAAGITATIGGAGIACIGIGAAAGAGITCGICAIGAA 153
                                                                                                                                                                                                                                                                                                                                                    154 GITTACCCAAAGGACTITACTATGTGAATTAAATTGTCAAACTAGTGGTCAGATCAATAA 213
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                                                                                                                                            13.2%; Score 31.4; DB 4; Length 29793; llarity 51.0%; Pred. No. 7.8; Conservative 0; Mismatches 71; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21068 TTTAATTTTTGAAAAAAAAAAA 21044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 AATTCTACGTGGCAAAAAAAAAA 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 38, Application US/09511477
Patent No. 6337202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Caenorhabadítis elegans
                        TYPE: DNA ORGANISM: Caencrhabaditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: JACOBSON, Myron K.
APLICANT: JACOBSON, Elaine L.
APLICANT: AME, Jean-Christophe
APPLICANT: LIN, Winston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 38
SEQ ID NO 38
LENGTH: 29793
                                                                                                                                                  Query Match
Best Local Similarity
Matches 74; Conservat
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US-09-511-477-38/c
LENGTH: 29793
                                                                           ; FEATURE:
US-09-302-812-38
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APELICANT: CACCOBON, Elaine L.
APELICANT: JACOBSON, Elaine L.
APELICANT: ACCOBSON, ELICANDE CONTROL EN TITLE OF INVENTION: THE PROPEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNORBACTIVE FILLE OF INVENTION: THEREWITH
FILLE OF INVENTION: THEREWITH
FILLE PLILAGE DATE: 1999-04-30
EARLIER APPLICATION NUMBER: 60/083,768
EARLIER PILLAGE DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 38
                                                                                                                                                                                                          APPLICANT: Inselburg, J. et al.
IIILE OF INVENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIFARUM
IIILE OF INVENTION: AND USES THEREFOR
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  3900 GIATTATGSCAGATGAGAIGGGACTTGGTAAGACACTTCAATGTATTGCTTTGT 3953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.2%; Score 31.4; DB 4; Length 6124; 47.3%; Pred. No. 4.3;
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                                                                                                                                                                                                                                                                                    FILE REFERENCE: JII-002CNCP
CURRENT APPLICATION NUMBER: US/08/213,419B
CURRENT FILING DATE: 1994-03-14
PRIOR APPLICATION NUMBER: US 07/870,506
PRIOR FILING DATE: 1992-04-17
NUMBER OF SEC ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 38, Application US/09302812B
Patent No. 6333148
GENERAL INFORMATION:
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                                                                                                 7.5-08-213-419B-3/c
; Sequence 3, Application US/08213419B
: Patent No. 6333406
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Matches 95; Conservative
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LOCATION: (2598)..(3404)
NAME/KEY: CDS
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NAME/KEY: CDS
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LENGTH: 6124
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278 AIGCITITTAAAATCCWAAACTAATATCAGTAGCCATGGAGTCATCGGCTTGAGG 219
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OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                    EARLIER APPLICATION NUMBER: 60/051,928
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/055,722
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
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EARLIER FILING DATE: 1997-08-18
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EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,661
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APPLICATION NUMBER: 60/055,947
FILING DATE: 1997-08-18
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BARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 66/056,360
BARLIER APLICATION NUMBER: 66/056,360
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SARLIER FILING DATE: 1997-08-18
SARLIER APPLICATION NUMBER: 60,055,984
EARLIER FILING DATE: 1937-08-18
EARLIER APPLICATION NUMBER: 60,055,954
EARLIER PILING DATE: 1997-08-18
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EARLIER APPLICATION NUMBER: 60/058,785
                                                                 FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,928
                              APPLICATION NUMBER: 60/051,919
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FILING DATE: 1997-08-18
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OTHER INFORMATION: n equals a,t,g,
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Best Local Similarity 50.74
Matches 72; Conservative
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ORGANISM: Homo sapiens
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LOCATION: (605)
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                    TITLE OF INVENTION: GENES ENCODING SEVERAL POLY (ADP-RIBOSE) GLYCCHYDROLASE (PARG) EN TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIV TITLE OF INVENTION: THEREWITH
FILE REFERENCE: NIAD 201
CURRENT APPLICATION NUMBER: US/09/511,507
CURRENT FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 09/302,812
PRIOR FILING DATE: 1999-34-30
NUMBER OF SEQ ID NCS: 38
SEC ID NO 38
LENGTH: 29793
TYPE: DATA
ORGANISM: Caenorhabaditis elegans
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13.2%; Score 31.4; DB 4; Length 29793;
Best Local Similarity 51.0%; Pred. No. 7.8;
Matches 74; Conservative 0; Mismatches 71; Indels 0;
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CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1999-07-07
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
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APPLICATION NUMBER: 60/052,795
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Patent No. 6342581
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APPLICANT: Fischer et al.
LIN, Winston
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ULIDAR INFORMATION: I equals a, t, c, or g
NAME/KET: misc feature
LOCATION: (30958)...(30938)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KET: misc feature
LOCATION: (309418)...(309418)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KET: misc feature
LOCATION: (312837)...(312837)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KET: misc feature
LOCATION: (312933)...(312933)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KET: misc feature
LOCATION: (312933)...(312933)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KET: misc feature
LOCATION: (312926)...(319226)
OTHER INFORMATION: n equals a, t, c, or g
OTHER INFORMATION: n equals a, t, c, or g
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (10398). (10398)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (148948). (148948)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (163385). (163385)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (191989). (191989)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (191995). (191995)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (231980). (231980)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (234187).. (234187)
COTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (234187).. (234187)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (234187).. (234220)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (234187).. (234814)
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LOCATION: (234187).. (234814)
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LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (98266)..(98266)
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OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
NAME/KEY: (60092)...(60092)
OTHER INFORMATION: n equals a, t,
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                                                                             NAME/KSY: misc_feature_
LOCATION: (98120). (98120)
OTHER INFORMATION: n equals a, t,
NAME/KSY: misc_feature
LOCATION: (38159). (98159)
OTHER INFORMATION: n equals a, t,
                            LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (98239)..(98239)
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LOCATION: (98343). (983
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(84812)..(848
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APPLICANT: Bult et al.
APPLICANT: Bult et al.
APPLICANT: Bult et al.
APPLICANT: Bult et al.
TITE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ Patent No. 6503729
TITE OF INVENTION: jannaschii
TITE OF INVENTION: jannaschii
TITE OF INVENTION: jannaschii
CURRENT APPLICATION NUMBER: US/08/916,421B
TITE OF SEPTION NUMBER: US/08/916,421B
PRIOR FILING DATE: 1997-06-22
NUMBER OF SEQ ID NOS: 3
                                                              Sequence 149, Application US/09601196

Fatent No. 6531583

FAREAL INFORMATION:
APPLICANT: Cassell H.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, John I.
APPLICANT: Glass, John I.
APPLICANT: Hainer, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: HEKWHITON: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA, TITLE OF INVENTION NUMBER: US/09/601,198
CURRENT FILING DATE: 2000-12-08
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-01-30
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LOCATION: (128222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LCCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c, or g
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US-08-916-421B-1/c
Sequence 1, Application US/08916421B
Patent No. 6503729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Ureaplasma urealyticum US-09-601-198-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin version 3.1
SEQ 1D NO 1
LENGTH: 1664976
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SEQ ID NO 149
LENGTH: 2244
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hes 59; Conserva
                                                            US-09-601-198-149
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CTHER INFORMATION: n equals a, t, c, or g
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OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
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LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t,
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LOCATION: (871519)..(871619)
OTHER INFORMATION: n equals a, t,
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OTHER INFORMATION: n equals a, t,
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LOCATION: (113081)...(1130881)
OTHER INFORMATION: c.equals a, t,
NAME/KET: misc feature
LOCATION: (1310988)...(1310988)
OTHER INFORMATION: n.equals a, t,
NAME/KEY: misc feature
LOCATION: (1313224)...(1313224)
OTHER INFORMATION: n.equals a, t,
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OTHER INFORMATION: n equals a,
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LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a,
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LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a,
          NAME/KEY: misc feature
LOCATION: {657203}..(657203)
OTHER INFORMATION: n equals a,
                                                          NAME/KEY: misc feature
LOCATION: (674435) ..(674435)
OTHER INFORMATION: n equals a,
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LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
NAME/XEY: misc feature
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OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
MIHER INFORMATION: n equals a,
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LOCATION: (1084830)..(1084830)
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LOCATION: (1349491)..(1349491)
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LOCATION: (1569020)..(1569020)
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LOCATION: (779676)..(779676)
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                                                                                                                                                                                                                                                                                                                                                                           619728 AATGATAAATTTTAGTCTACGAAGGTTCTATCAAGATGATATTATAAAAAACTACA 619672
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                                                                                   1 TITITITITITITIGGGAGGAAATCACGGCGGCGGATGCAACAGTCTTCTCTCTAATTGGCA
                                              0; Gaps
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12.9%; Score 30.6; DB 4; Length 1664976; 45.6%; Pred. No. 56; Live 0; Mismatches 129; Indels 0; C
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APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455611
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6426072
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OTHER INFORMATION: n = A,T,C or G
US-09-643-597-266
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Fan, Liqun
Kalos, Michael D.
Bangur, Chaitanya S
Hosken, Nancy
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Li, Samuel X.
Wang, Aijun
Skeiky, Yasir A.W.
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Best Local Similarity 49.73
Matches 76; Conservative
                                              108; Conservative
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ORGANISM: Homo sapien
                        Best Local Similarity
Matches 108; Conserva
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US-09-643-597-266/c
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RESULT 13 US-09-480-884A-266/c

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83 ATCACATITICGGAIGITCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAG 142
                                                             181 ATTACAAAATGATTGTATTTAAAGAATTTTTAAAATCCAGAAGTCATTTAAATAG 122
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Job time : 87 secs
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LOCATION: (1)...(401)
CTHER INFORMATION: n = A,T,C or G
US-09-606-421B-266
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
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Best Local Similarity 49.74
Matches 76; Conservative
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ORGANISM: Homo sapien
FEATURE:
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US-09-606-421B-266/c
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US-09-542-6;5A-266/c
; Sequence 266, Application US/095426;5A
; Patent No. 6518256
; Patent No. 6518256
; Renaral INFORMATION:
    APPLICANT: Wang, Tongtorg
; APPLICANT: Ralos, Michael D.
; APPLICANT: Ralos, Michael D.
; APPLICANT: Hosker, Nancy A.
; APPLICANT: Panger, Gary R.
; APPLICANT: Panger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; TITLE OF INVENTION: NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PartSEQ for Windows Verein 1.
                                                                APELICANT: Wang, Tongtong
APELICANT: Wang, Tongtong
APELICANT: Wang, Tongtong
APELICANT: Backen, Mancy A.
APELICANT: Backen, Mancy A.
APELICANT: Ralos, Michael D.
APELICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C6
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DAIE: 2001-08-27
NUMBER OF SEC ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
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Sequence 266, Application US/09480884A Patent No. 6482597
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p OTHER INFORMATION: n = A,T,C or G
US-09-542-615A-266
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; OTHER INFORMATION: n = A,T,C or G
US-09-48C-884A-266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CRGANISM: Homo sapien
                                              GENERAL INFORMATION:
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143 ITCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGAATTAAATTGTCAAACTAGTAGT 202
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                                                        121 BACCICATATAGTATGAACHATAAAATATTTTACATTTCATGAAATTTTTGCTGT 62
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APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
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CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 266
LENGTH: 401
                                                                                                                                                                                                                                                                                                                                                     Sequence 266, Application US/09606421B Patent No. 6531315 GENERAL INFORMATION:
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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SUMMARIES

Description	Sequence 49714, B	Seguence 49714, A	Sequence 135, App	Sequence 87384, A	Sequence 94282, A	Sequence 305384,	Sequence 94282, A	Sequence 305384,	Sequence 17073, A	Sequence 5790, Ap	Sequence 1659, Ap	Sequence 358, App	Sequence 13, Appl	Sequence 13, Appl
ΙD	US-10-085-783A-49714	US-10-242-535A-49714	US-10-041-018-135	US-10-424-599-87084	US-10-027-632-94282	US-10-027-632-305384	US-10-027-632-94282	US-10-027-632-305384	US-09-918-995-17073	US-09-783-590-5790	US-10-311-455-1659	US-09-770-149-358	US-09-764-855-13	US-10-072-349-13
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% Query Match	15.5	15.5	15.2	14.4	14.4	14.4	14.4	14.4	14.0	14.0	13.9	13.8	13.8	13.8
Score	37	33	36.2	34.2	34.2	34.2	34.2	34.2	33.4	33.4	33.2	32.8	32.8	32.B
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49 TGGTAAAGATTGATTATAGTTACTCATTTTATCTTAAATGGAGTTTAAGTAAAGTTG 108

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56 TOSCAACTGTCTATTATCCATTCCCAATCACATTTCGGATGTTCTCGAAAAGGACTTCC

109 CTTTGCCTTGATAGAATTGTAACAICAIGCTCCAAGAAATATAATICCAATAATTTACTA 168

116 CAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCAAAGGACTTTACTA

15 16 US-10-398-221-3612 Sequence 31, Appl 18 13 US-10-242-485-43 Sequence 41, Appl 18 13 US-10-172-118-765 Sequence 765, App 13 US-10-172-118-765 Sequence 765, App 19 Sequence 765, App 19 Sequence 765, App 19 Sequence 765, App 19 Sequence 58, Appl 19 US-10-175-523-61 Sequence 61, Appl 19 US-10-175-523-61 Sequence 61, Appl 19 US-10-175-523-61 Sequence 79, Appl 19 US-10-175-523-79 Sequence 79, Appl 19 US-10-175-523-79 Sequence 224261, Appl 19 US-10-175-523-24261 Sequence 79, Appl 19 US-10-175-523-19 Sequence 224261, Appl 19 US-10-193-193-194-4562 Sequence 224261, Appl 19 US-10-193-1944-4562 Sequence 589, Appl 19 US-10-193-1944-4562 Sequence 589, Appl 19 US-10-193-1944-4562 Sequence 589, Appl 19 US-10-193-1944-4562 Sequence 589, Appl 19 US-10-194-197-239-37 Sequence 187, Appl 19 US-10-194-197-239-37 Sequence 589, Appl 19 US-10-194-197-239-37 Sequence 589, Appl 19 US-10-194-197-239-30 Sequence 589, Appl 19 US-10-194-197-239-30 Sequence 187, Appl 19 US-10-194-195-2147 Sequence 187, Appl 19 US-10-194-195-2147 Sequence 187, Appl 19 US-10-194-195-2147 Sequence 1194, Appl 19 US-10-194-195-2147 Sequence 2147, Appl 19 US-10-194-195-2147 Sequence 2147, Appl 19 US-10-194-195-2147 Sequence 2147, Appl 19 US-10-194-195-2147 Sequence 2147, Appl 19 US-10-194-196-194-194-194-194-194-194-194-194-194-194	re 37; DB 13; Length 263; d. No. 0.77; M.Smatches 75; Indels 0; Gaps 0;
16 US-10-399-2 18 US-10-240-4 19 US-10-172-1 15 US-10-175-5 15 US-10-175-5 15 US-10-175-5 15 US-10-175-5 15 US-10-175-5 15 US-10-176-5 16 US-10-176-5 17 US-10-176-5 18 US-09-973-2 19 US-09-973-2 19 US-09-973-2 19 US-09-973-2 19 US-09-973-2 19 US-09-973-2 19 US-09-973-2 10 US-09-973-2 11 US-09-973-2 12 US-09-973-2 13 US-09-973-2 14 US-09-973-2 15 US-09-973-4 15 US-09-973-4 16 US-10-987-7 17 US-10-987-7 18 US-09-973-4 19 US-09-973-4 19 US-09-973-4 10 US-	Sco Pre 0;
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Matches 57
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TITLE OF INVEXTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005 2009
FILE REFERENCE: 4231/2005 2009
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-09-12
PRIOR PLING DATE: 2001-07-13
PRIOR FILING DATE: 2010-07-13
PRIOR FILING DATE: 2010-07-13
PRIOR PLING DATE: 2010-07-13
PRIOR FILING DATE: 2010-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR PLING DATE: 2010-03-12
PRIOR PLING DATE: 2010-03-12
PRIOR FILING DATE: 2001-02-28
PRIOR PLING DATE: 2001-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.5%; Score 37; DB 16; Length 263; 52.2%; Pred. No. 0.77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 135, Application US/10041018
Publication No. US20040072323A1
GENERAL INFORMATION:
APPLICANT: Matsuda, Selichi P.T.
APPLICANT: ATT, Elizabeth A.
TITLE OF INVENTION: Diterpene-Producing Unicellular Crganism
FILE REFERENCE: P02080US1/10025547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75; Indels
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176 TGTGAATTAAATTGTCAAACTAGTAGTCAGATCAATA 212
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                                                                        169 maaaasmaammaaaacmmamemaammaaca 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259880
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ 1D NOS: 413
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                             ; Sequence 49714, Application US/10242535A; Publication No. US20040013663A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.2 SEQ ID NO 49714
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ORGANISM: Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ChondroGene Inc.
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Best Local Similarity
Matches 82; Conserv
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ORGANISM: Human
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Sequence 87084, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION TOWNER: US/10/424,599
CURRENT FILE OF THE OFTEN TOWNER: US/10/424,599
CURRENT FILE OFTEN TOWNER: US/10/424,599
SEQ ID NOS: 285684

SEQ ID NOS: 285684
                                                                236 ACTICTCAGTITICATAAAGTATAGGGATGGAATICTAAATTAAACCTTTTTAACTCAAA 295
                                                                                                                                                                                     296 TAAGTAAATTCAAAATTCCAGAAATTAAAAACAGAAAAATTAAATTTCAAAAGTATGA 355
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110 ACTICCCAAAGITATIGGAGTACIGIGAAAGAGITCGICAIGAAGITTTACCCAAAGGACT 169
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.123
CURRENT PELICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/165,358
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/165,358
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-109-28
                                                                                                                                          170 TIACIAIGIGAATIAAAITGICAAACIAGIAGICAGAICAAIAAAITCIACGIGGCAAA
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Pred. No. 5.6;
C; Mismatches 38; Indels 0.
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; OTHER INFORMATION: Clone ID: PAT MRT3847_49647C.1
US-10-424-599-87084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 AGAICAAIAAAIICIACGIGGCAAAAAAAAAAA 238
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57; Conservative
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ORGANISM: Glycine max
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RESULT 8
US-10-027-632-305384/c
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ORGANISM: Human
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### TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
### TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
### TITLE OF INVENTION: Polymorphisms in the Human Genome
### TITLE OF INVENTION: Polymorphisms in the Human Genome
### CURRENT APPLICATION NUMBER: US/10/027,632
### CURRENT APPLICATION NUMBER: US 60/18,066
### PRIOR APPLICATION NUMBER: US 60/18,066
### PRIOR FILING DATE: 2000-04-20
### PRIOR FILING DATE: 2000-02-24
### PRIOR FILING DATE: 2000-03-29
### PRIOR FILING DATE: 1999-11-23
### PRIOR APPLICATION NUMBER: US 60/165,368
### PRIOR APPLICATION NUMBER: US 60/165,368
### PRIOR PLING DATE: 1999-09-28
### PRIOR FILING DATE: 1999-09-28
### PRIOR FILING DATE: 1999-09-28
### PRIOR FILING DATE: 1999-09-28
### PRIOR FILING DATE: 1999-09-28
### PRIOR FILING DATE: 1999-09-28
### PRIOR FILING DATE: 1999-09-28
### PRIOR FILING DATE: 1999-09-09
### NUMBER OF SEQ ID NOS: 325720
### SASSAG FOR WINDOWS VETSION 4.0
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                                                                                                                                                                                                                                                       Length 614;
                                                                                                                                                                                                                                                     14.4%; Score 34.2; DB 13; Length 64.6%; Pred. No. 7.7; tive 0; Mismatches 28; Indels
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 94282
LENGTH: 614
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US-10-327-632-94282/c
Sequence 94282, Application US/10027632; Publication No. US2003020407589
                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 ACGTGGCAAAAAAAAA 238
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Best Local Similarity 64.63
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                     51; Conservative
                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 51; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-10-027-632-305384/c
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                                                                                                                                                    TYPE: DNA
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TITLE OF INVESTION: Lear-ification and Mapping of Single Mucleotide
FILIS OF INVESTION: Lear-ification and Mapping of Single Mucleotide
FILIS OF INVESTION: Lear-ification and Mapping of Single Mucleotide
FILIS OF INVESTION: Lear-ification and Mapping of Single Mucleotide
FILIS OF INVESTION: DATE: 2002-04-30
FILIS OF INVESTION: DATE: 2002-04-30
FILIS OF INVESTION: MARKET SINGLE MACLEOTICE
FILIS OF INVESTION: MARKET SINGLE MACLEOTICE
FILIS OF INVESTION: MARKET SINGLE MACLEOTICE
FILIS OF INVESTION: MARKET SINGLE MACLEOTICE
FILIS OF INVESTION: MARKET SINGLE MACLEOTICE
FILIS OF INVESTION: MARKET SINGLE MACLEOTICE
FILIS APPLICATION WINNESS: US 60/156,358
FRICE FILING DATE: 2002-02-24
FRICE FILING DATE: 2002-02-24
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FRICE FILING DATE: 2002-02-24
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FRICE FILING DATE: 2002-02-24
FRICE FILING DATE: 2002-03-26
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CURRENT APPLICATION NUMBER: US/09/783,590
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LOCATION: (395)
OTHER INFORMATICN: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or
                         CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12465
SCFTWARE: PatentIN Ver. 2.0
ISSC ID NO 5790
LENGTH: 499
                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (9)
CTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (127)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (262)
OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (346)
OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (330)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (337)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
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LOCATION: (302)
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                                                                                                                                                                                                                                                                                                     CREANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                                                                                            160 CCAAAGGACTTTACTATGTGAATTAAATTGTCAAACTAGTAGTCAGATCAATAAAATTCT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 AAGGACTICCCAAAGTIATIGGAGTACTGTGAAAGAGTICGTCATGAAGTITACCCAAAG 165
                                                                                                                                                                                                             180 CCCAATSTRGTCCTAATGTTAATTAAATATAAGAAGGCAGAAGAAGAATAAATTAAT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 ITCTCTCAATTGGCAACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 indigiananingackagarichtrianaachaagaaarriaarithtrinighachagaa 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 AMMANITIGAACAITITIAGITCITIGGITATAAAATGITAATITCAGAA--TIAGITITAAT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 GACTITACTATGTGAATTAAATTGTCAAACTAGTAGACAGATCAATAAAATTCTACGTGG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279 GCCTTAATTAAACTAATTAATAGCTTTGGACACTTAAAAGAGCTCTAAATTTGCTTGTAA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Li, Handong
APPLICANT: Li, Handong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
ITILE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
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                                                                                                            Gaps
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                                                Query Match
Best Local Similarity 64.6%; Pred. No. 7.7;
Matches 51; Conservative 0; Mismatches 28; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
14.0%; Score 33.4; DB 10; Length 404;
Best Local Similarity 51.8%; Pred. No. 11;
Matches 100; Conservative 0; Mismatches 91; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-918-995-17073

Sequence 11073, Application US/09918995

Publication No. US2030073623A1

GENERAL INPORATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: PROM VARIOUS CDNA LIBEARIES

TITLE OF INVENTION: PROM VARIOUS CDNA LIBEARIES

TITLE OF INVENTION: PROM VARIOUS CDNA LIBEARIES

TITLE OF INVENTION: DOUGL NOVEL US/09/918, 995

CURRENT APPLICATION NUMBER: US/09/918, 995

CURRENT FILING DATE: 1999-01-20

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE FASTSEQ for WINGOWS Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) LOCATION: (1)...(404)

; OTHER INFORMATION: n = A,T,C or G

US-09-918-995-17073
                                                                                                                                                                                                                                                                      220 ACGTGGCAAAAAAAAAA 238
                                                                                                                                                                                                                                                                                                                         120 ATGTGACAACAAAACAGA 102
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APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 CAAAAAAAAAA 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-09-783-590-5790/c
US-10-027-632-305384
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LENGTH: 404
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APPLICANT: PIEPERBROCK, Christian
APPLICANT: PIEPERBROCK, Christian
APPLICANT: BERLIN, Kurt
ITILE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Dete:
ITILE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: 1014
CURRENT APPLICATION NUMBER: 1016
CURRENT APPLICATION NUMBER: ECT/EPO1/07537
PRIOR APPLICATION NUMBER: ED 1032523.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TIATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 TIATATAATAACTITAATAATAATAACTITTAAATAACTITTAAATAACTITATTATAACTA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 8781;
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APPLICANT: Allen, Keith R.
APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Neith
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Explainan
FILE REFERENCE: 2024 (PARA-019RV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 13.9%; Score 33.2; DB 15;
1 Similarity 55.1%; Pred. No. 52;
65; Conservative 0; Mismatches 53;
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SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 358
LENGTH: 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 358, Application US/09770149
Patent No. US20020059653A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
APPLICANT: An. Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
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Woessner, Jeffrey P.
Haas, William David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page, Amy
Matthew, Abraham V.
  Publication No. US20030143606Al
GENERAL INFGRMATION:
APPLICANT: OLEK, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Seguence
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Rameaka, Joshua G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kricker, Maja
Slader, Ted
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Best Local Similarity
Matches 65; Conserv
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US-09-770-149-358/c
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281 CTACTAATAACNCCAAAATNAAATTTAATAACTCTACTACAGGGGCTTNCCACTTTTTCA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 GGAGTACTGTGAAAGAGTTCGTCATGAAGTTTTACCCAAAGGACTTTACTATGTGAATTAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 TAAGTIGITANCAACATTITIGGITTATICAGAACATCTAACAGCATGTTCTAA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 ATGTTCAAATTAAAAGGTAATTACATGAAAT 131
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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US-10-311-455-1659/c
; Sequence 1659, Application US/10311455
                                                                          LOCATION: (398)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (408)
OTHER INFORMATION: n equals a,t,g,
                 LOCATION: (396)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                             LCCATION: (439)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                       LOCATION: (423)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                         LOCATION: {417}
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (468)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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Matches 76; Conservative
WAME/KEY: misc feature
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NAME/KEY: misc feature
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LOCATION: (492)
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                                                                          13.8%; Score 32.8; DB 9; Length 678; ilarity 64.5%; Pred. No. 21; Conservative 0; Mismatches 27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PAIIO
CURRENT APPLICATION NUMBER: US/09/764,855
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 334
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SITE
LOCATION: (1)
OTHER INPORMATION: n equals a, L, g, or c
NAME/KEY: SITE
LOCATION: (56)
OTHER INFORMATION: n equals a, L, g, or c
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/09764855
Patent No. US20020119919A1
GENERAL INFORMATION:
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OTHER INFORMATION: n equals a,t,g,
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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FEATURE:
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Matches 52; Conserv
                                                                                            Best Local Similarity
Matches 49; Conserv
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LOCATION: (687)
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US-09-754-855-13/c
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RESULT 14 US-10-072-349-13/c

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153 AGTTTACCCAAAGGACTTTACTATGTGAATTAAATTGTCAAACTAGTAGTCAGATCAATA 212
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Sequence 3432, Application US/10398221;
Publication No. US20040018514A1
GENERAL INPORMATION:
APPLICANT: KUNST, Frederik
FALE REPREMENTON:
FILE REPREMENT ENASRE, Philippe
FILE OF INVENTION: Listeria innocua, genome and applications
FILE REPREMENT ENA 702 - US
CURRENT FILING DATE: 2003-03-27
PRIOR PILING DATE: 2003-03-27
PRIOR PLING DATE: 2001-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOTWARE: PatentIn version 3.0
SEQ ID NO 3632
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Pred. No. 22;
0; Mismatches 34; Indels 0;
                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PALIOCI
CURRENT APPLICATION INVERE: US/10/072,349
CURRENT FILING DATE: 2002-02-11
Prior Application removed - See file Wrapper or Palm
NUCLEAR OF SEQ ID NOS: 334
SOCTWARE: Patentin Ver. 3.1
SEQ ID NO 13
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (687)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g, or NAME/KRY: misc feature
LOCATION: (397)

OTHER INFORMATION: n equals a,t,g, or NAME/KRY: misc feature
1.0CATION: (512)
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ORGANISM: Listeria monocytogenes 4b
Sequence 13, Application US/10072349
Publication No. US20030054420A1
GENERAL INFORMATION:
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ilarity 60.5%;
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ORGANISM: Homo sapiens
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US-10-398-221-3632
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### FEATURE:
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